

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2005, 17:11:04 ; Search time 7197 Seconds  
(without alignments)

11847.153 Million cell updates/sec

Title: US-09-544-776-1

Perfect score: 2240

Sequence: 1 cgtcacacagtaggtccct.....taaaaaaaaaaaaaaaaaa 2240

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	41.8	1.9	46	1 AA995439	AA995439 0884f01.8
2	36	1.6	50	1 AU104978	AU104978 AU104978
3	36	1.6	50	1 AU104979	AU104979 AU104979
4	36	1.6	50	1 AU104981	AU104981 AU104981
5	36	1.6	50	1 AU104985	AU104985 AU104985
6	34.4	1.5	50	1 AU104974	AU104974 AU104974
7	34.4	1.5	50	1 AU104977	AU104977 AU104977
8	34.4	1.5	50	1 AU104980	AU104980 AU104980
9	34	1.5	50	1 AU104976	AU104976 AU104976
10	33.8	1.5	37	8 AZ761912	AZ761912 1M0556D02
11	33	1.5	50	1 AU104983	AU104983 AU104983
C 12	32.2	1.4	45	8 AZ843544	AZ843544 2M0142022
13	32	1.4	50	1 AU104984	AU104984 AU104984
14	32	1.4	50	1 AU104986	AU104986 AU104986
C 15	30.8	1.4	50	9 BX976589	BX976589 Forward 8
16	30.2	1.3	43	8 AZ419099	AZ419099 1M0195N23
17	29.6	1.3	37	8 AZ332980	AZ332980 1M0155P13
18	29.6	1.3	37	8 AZ623276	AZ623276 1M0460M16
19	29.6	1.3	48	8 AZ443723	AZ443723 1M0238D11
20	29.2	1.3	43	7 H41505	H41505 yp68h12.s1
21	29.2	1.3	50	1 A1252059	A1252059 gw39f04.x
C 22	28.8	1.3	49	8 AZ840678	AZ840678 2M0138O16
23	28.6	1.3	36	8 AZ479840	AZ479840 1M0300P16
24	28.6	1.3	49	2 BF789094	BF789094 602104956

#### ALIGNMENTS

RESULT 1  
AA995439/c  
LOCUS  
DEFINITION  
O884f01.81 NCI CGAP GC2 Homo sapiens CDNA clone IMAGE:1612057 3'  
similar to TR:Q90637 Q90637 CHS-REX-S. i, mRNA sequence.  
AA995439  
VERSION  
AA995439.1 GI:3181928  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 46)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,  
Ph.D.

CDNA Library Arraying: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1604 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.

#### FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1612057"  
/tissue\_type="germ cell tumor"  
/lab\_host="SOLR (kanamycin resistant)"  
/notes="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; Cloned unidirectionally. Primer: Oligo dT. Bulk  
germ cell tumor. 5' adaptor sequence: 5' GAATTCGACGAG 3'  
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'  
Average insert size: 1.2 kb."

CG731182 1119136A0  
AZ792853 2M0045C07  
AU103294 AU103294  
AZ435186 1M0222E03  
CD577044 IgoR3\_C01  
CR430378 CR430378  
AZ627160 1M0467L09  
BF107886 601823895  
AA145482 mr62a06.r  
AA590944 mr25f02.r  
AZ68544 2M0240J20  
AZ407440 1M0178H1S  
BI491464 df09f10.w  
CV304274 tg94g02.b  
AZ358097 1M0100N08  
AZ816605 2M0085K24  
AZ861629 2M0168A19  
AZ942114 2M0202F08  
AZ967786 2M0238F20  
CR003825 Forward 8  
CR048038 Reverse 8

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32 8 AZ792853  
50 1 AU103294  
33 8 AZ435186  
50 6 CD577044  
50 7 CR430378  
50 8 AZ627160  
47 2 BF107886  
49 1 AA145482  
50 1 AA590944  
44 8 AZ68544  
49 8 AZ407440  
50 7 CV304274  
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50 8 AZ942114  
50 8 AZ967786  
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50 9 CR048038

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## ORIGIN

Query Match 1.9%; Score 41.8; DB 1; Length 46;  
 Best Local Similarity 95.6%; Pred. No. 2e+02;  
 Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1060 TATTACCTATGTGTGCTGCTTGTAAATGCTGACACTACTGA 1104  
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 Db 45 TATTACCTATGTGTGCTGCTTGTATTGCTGACACTACTGA 1

## RESULT 2

AU104978  
 LOCUS AU104978 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION AU104978 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 CAS06347, mRNA sequence.

ACCESSION AU104978 GI:13554499

VERSION AU104978

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL 21270072

MEDLINE 11375929

PUBMED

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

## FEATURES

source

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGGCCCA 36

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Db 15 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGGCCCA 50

## RESULT 3

AU104979  
 LOCUS AU104979 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION AU104979 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 CAS08333, mRNA sequence.

ACCESSION AU104979 GI:13554500

VERSION AU104979

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,  
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and  
 Sugano,S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

## FEATURES

source

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 1.6%; Score 36; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGGCCCA 36

|||||

Db 15 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGGCCCA 50

## RESULT 4

AU104981  
 LOCUS AU104981 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION AU104981 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 HRC03106, mRNA sequence.

ACCESSION AU104981 GI:13554502

VERSION AU104981.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL 21270072

MEDLINE 11375929

PUBMED

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

## FEATURES

source

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="Sugano Homo sapiens cDNA library"

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Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 36
Db 15 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 50

RESULT 5
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LOCUS
DEFINITION
AUI04985 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI01927, mRNA sequence.
ACCESSION
AUI04985
VERSION
AUI04985.1 GI:13554506
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
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/db_xref="taxon:9606"
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Best Local Similarity 97.2%; Pred. No. 8.8e+03;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 36
Db 15 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 50

RESULT 7
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LOCUS
DEFINITION
AUI04977 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS03274, mRNA sequence.
ACCESSION
AUI04977
VERSION
AUI04977.1 GI:13554498
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
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Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 36
Db 15 CGTCACACAGTAGGTCCTCGGCTCAGTCGGGCCCA 50

RESULT 6
AUI04974
LOCUS
DEFINITION
AUI04974 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAE01363, mRNA sequence.
ACCESSION
AUI04974
VERSION
AUI04974.1 GI:13554495
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
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/clone="CAE01363"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      1.5%; Score 34.4; DB 1; Length 50;
Best Local Similarity 97.2%; Pred. No. 8.8e+03;

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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 33.8; DB 8; Length 37;  
Best Local Similarity 94.6%; Pred. No. 1.1e+04;  
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 237 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 273  
Db 1 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 37

RESULT 11

AU104983 50 bp mRNA linear EST 28-JAN-2004  
LOCUS AU104983 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION HRC11726, mRNA sequence.

ACCESSION AU104983.1 GI:13554504

VERSION EST.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Oka, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

PUBLISHED 21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

Email: [yszuk@iims.u-tokyo.ac.jp](mailto:yszuk@iims.u-tokyo.ac.jp)

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. 50

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HRC11726"

/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 1.5%; Score 33; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

5 ACCACAGTAGGTCCTCGGCTCAGTCGGCCAG 37

18 ACCACAGTAGGTCCTCGGCTCAGTCGGCCAG 50

Db

RESULT 12

AZ843544/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Plasmid insert

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

University of Utah

Em. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000

Std Error: 0.00

Plate: 0142

row: 0

column: 22

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. 45

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0142022"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.4%; Score 32.2; DB 8; Length 45;

Best Local Similarity 91.9%; Pred. No. 2.6e+04;

Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORIGIN

Query Match 1.4%; Score 32.2; DB 8; Length 45;  
Best Local Similarity 91.9%; Pred. No. 2.6e+04;  
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:13:52 ; Search time 4324 Seconds  
(without alignments)  
4179.879 Million cell updates/sec

Title: US-09-544-776-2  
Perfect score: 1910  
Sequence: 1 MEDLDSPVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRAE 373

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=Genembl -QFMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
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Database : GenEmbl.\*  
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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1879	98.4	1122	6	BD249448
2	1879	98.4	1122	9	HSA251384
3	1879	98.4	1485	9	BC010737 Homo sapi
4	1879	98.4	1610	6	BD231889

5	1879	98.4	1619	9	AK129806
6	1879	98.4	1654	9	BC012619
7	1879	98.4	1668	9	BC026788
8	1879	98.4	1709	9	AB040463
9	1879	98.4	1728	9	BC068991
10	1879	98.4	2235	9	AF148538
11	1879	98.4	2276	9	AF132047
12	1879	98.4	2332	9	AF102277
13	1876	98.2	1525	9	AK130812
14	1875	98.2	1599	6	CQ769577
15	1871	98.0	2052	9	AB015639
16	1862	97.5	1694	6	CQ783030
17	1862	97.5	1694	6	BD127437
18	1862	97.4	1694	9	AK075039
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20	1859	97.4	2389	9	AY102278
21	1717	89.9	1466	9	BC071848
22	1584.5	83.0	2156	10	AY164740
23	1584.5	83.0	2156	10	RN0242962
24	1584.5	83.0	2410	10	BC070879
25	1568.5	82.1	2256	10	AF132046
26	1566	82.0	2782	6	AX700396
27	1566	82.0	2782	10	AY164741
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31	1542	80.7	2266	10	AY102282
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Protein similar to neuroendocrine-specific protein, and encoding  
BD249448  
cDNA.  
ACCESSION BD249448  
VERSION BD249448.1 GI:33059218  
KEYWORDS JP 2002522016-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1122)  
AUTHORS Michalovich, D. and Prinjha, R.K.  
TITLE Protein similar to neuroendocrine-specific protein, and encoding  
JOURNAL Patent: JP 2002522016-A 3 23-JUL-2002;  
SMITHKLINE BEECHAM PLC  
COMMENT OS Homo sapiens (human)  
PN JP 2002522016-A/3  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310  
PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB 9916898.1 PI  
DAVID MICHALOVICH,RABINDER KUMAR PRINJHA  
PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
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## Alignment Scores:

Pred. No.:	2,97e-67	Length:	1122
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Best Local Similarity:	99.20%	Mismatches:	3
Query Match:	98.38%	Indels:	0
DB:	9	Gaps:	0
US-09-544-776-2 (1-373) x HSA251384 (1-1122)			
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QY	21	ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu	40
DB	61	CCCGGCTTCAAGTACCAAGTCTGCTGAGGAGCCCGAGGAGGAGGAGGAGGAG	120
QY	41	GluGluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGlu	60
DB	121	GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	180
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QY	81	PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal	100
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QY	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
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QY	141	AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
DB	421	GCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
QY	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly	180
DB	481	CCGCGAGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGC	540
QY	181	SerSerGlySerValValValValValValValValValValValValValValVal	200
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QY	301	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	320

Db	901	AACTTTCAGTGTGTGATGTGGGTATTTACCATGTGTGGTGCCTGTTTAAATGCTGTGACA	960
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DB	961	CTACTGATTTGGCTCTCTCATTTCACTTCTTCAGTGTTCCTGTTATTTATGACGGCATCAG	1020
QY	341	AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys	360
DB	1021	GCACAGATAGATCATTTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAA	1080
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DEFINITION	Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone IMAGE:3901353), complete cds.		
ACCESSION	BC010737		
VERSION	BC010737.1		
KEYWORDS	GI:14789600		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1485)		
AUTHORS	Strausberg, R.D., Collins, F.S., Wagner, L.H., Grouse, L.H., Dege, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, R., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1485)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www-ahgc.stanford.edu">http://www-ahgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 14 Row: n Column: 2  
This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF analysis  
This clone has the following problem: The cds is short compared to the longest cds in the locus.

## FEATURES

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Location/Qualifiers

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σπρε

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CD5

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## ORIGIN

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Query Match:	98.38%	Gaps:	0
DB:			9

US-09-544-776-2 (1-373) x BC010737 (1-1485)

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Best Local Similarity: 99.20% Mismatches: 3  
Query Match: 98.38% Indels: 0  
DB: Gaps: 0

US-09-544-776-2 (1-373) x BD231889 (1-1610)

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QY 21 ProAlaPheIysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
DB 192 CCCGCGTTCAAGTACCAGTTCTGTGAGGAGCCCGAGACGAGGAGGAAGAGGAGGAG 251  
QY 41 GluGluGluAspGluAspGluAspLeuGluGluGluGluGluGluGluGluGlu 60  
DB 252 GAAGAGGAGGACGAGGACGAGACCTGGAGAGCTGGAGGTCTGGAGGAGGAGCCCGCC 311  
QY 61 AlaGlyIleuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
DB 312 GCCGGGCTGTCCGCGCGCCAGTGCACCCGCGCCCTGCCCGCGCGCGCCCTGGTGGAC 371  
QY 81 PheGlyAsnAspPheValProAlaProAlaProArgGlyPheLeuProAlaAlaProVal 100  
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QY 201 ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 220  
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DEFINITION AK129806  
ACCESSION AK129806.1 GI:34526422  
VERSION oligo capping; fis (full insert sequence).  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1619)  
Sugano, S. and Suzuki, Y. Direct Submission  
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fldcna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.  
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ORIGIN  
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Pred. No.: 1879.00 Matches: 370  
Score:

Percent Similarity:	99.20%	Conservative:	0
Best Local Similarity:	99.20%	Mismatches:	3
Query Match:	98.38%	Indels:	0
DB:	9	Gaps:	0
US-09-544-776-2 (1-373) x AK129806 (1-1619)			
QY	1	MetGluAspLeuValSerProLeuValSerSerSerSerSerProProArgProGln	20
DB	158	ATGGAAGACCTGGACCAAGCTCTCTGGTCTCGTCTCGACAGCCACCCCGCGCGAG	217
QY	21	ProAlaPheLysTyrglnPheValArgGluProGluAspGluGluGluGluGlu	40
DB	218	CCGCGTTTCAGTACCAAGTTCGTGAGGAGCCCGAGGACGAGGAGGAGGAG	277
QY	41	GluGluGluAspGluAspGluAspLeuGluGluValLeuGluArgLysProAla	60
DB	278	GAAGAGGAGGACGAGGACCAAGACCTGGAGGAGCTGGAGGTCTGGAGAGGAGCCCGCC	337
QY	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
DB	338	GCCGGGCTGTCCGCGGCCCGACGTGCCCCACCGCCCTGCGCGCGCGCCCTGATGGAC	397
QY	81	PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal	100
DB	398	TTCCGNAATGATTTCTGTGCGCGCGCGGCCCGCGGAGACCCCTGCGCGCGCTCCCGCCGTC	457
QY	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
DB	458	GCCCCGAGCGGACCGCTTTGGGACCGACCGCGGTCTGTCGACCGTGGCCCGCCGCA	517
QY	121	SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluProPro	140
DB	518	TCCCCGCTGTCTGTCGCCAGTCTGCGCCCTCAAGCTCCCTGAGGACACGAGGCTCGG	577
QY	141	AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
DB	578	GCCCGGCTTCCCGCTCCTCCCGCGCCAGCGTGAGCCCCCAGGAGCCCGTGGACC	637
QY	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly	180
DB	638	CGCCGAGCCCGGCTCCCGCGCGCCCTCCACCGCGCGCGCCCAAGCGCAGGGGC	697
QY	181	SerSerGlySerValValValAspLeuLeuTyrrTrpArgAspIleIleIleIleIleIleIle	200
DB	698	TCCTCGGCTCAGTGTTGACCTCTCTGTTACTGGAGAGACATTAAAGAACTCGAGTG	757
QY	201	ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal	220
DB	758	GTGTTTGGTGCCAGCCTATTCTCGTGTCTTTTCATTGACAGATTTCAGCATTGTGAGCGTA	817
QY	221	ThrAlaTyrrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrrLysGly	240
DB	818	ACAGCGCTACATTGCTTGGCCCTGTCTCTGTGACCATCAGCTTTAGGATATACAGGGT	877
QY	241	ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSer	260
DB	878	GTGATCCAGCTATCCAGAAATCAGATGAAGCCACCCATTGAGGCAATTCGGAATCT	937
QY	261	GluValAlaIleSerGluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisVal	280
DB	938	GAAGTTGTATATCTCAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTTCTGTCATGTG	997
QY	281	AnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeu	300
DB	998	AACTGCAGATAAAGAACTCAGGCGCCCTCTTTCTAGTTGATGATTTAGTTGATTTCTCTG	1057
QY	301	LysPheAlaValLeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThr	320
DB	1058	AGTTTGCAGTGTGATGTTGGGATTTTACCTATGTTGGTCCCTGTTTAAATGCTGTGACA	1117
QY	321	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrrGluArgHisGln	340

Db	1118	CTACTGATTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATTATGAACGGCATCAG	1177
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Db	1178	GCACAGATAGATCATTAATCTAGGACTTGCAATAAAGATGTTAAAGATCTATGGCTAAA	1237
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RESULT 6			
LOCUS	BC012619	1654 bp	mRNA linear PRI 29-JUN-2004
DEFINITION	Homo sapiens reticulon 4, transcript variant 2, mRNA (cdna clone IMAGE:4082756), complete cds.		
ACCESSION	BC012619		
VERSION	BC012619.1	GI:15214977	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1654)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1654)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs@mail.nih.gov">cgapbs@mail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology <a href="http://www.systemsbio.org">http://www.systemsbio.org</a> contact: <a href="mailto:amadon@systemsbio.org">amadon@systemsbio.org</a> Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 19 Row: d Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932 This clone has the following problem: The cds is short compared to the longest cds in the locus.			
FEATURES	Location/Qualifiers 1..1654		
source			





TITLE	Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	DB:	9	Gaps:	0
JOURNAL	12477932	US-09-544-776-2 (1-373) x BC026788 (1-1668)			
PUBMED	2 (bases 1 to 1668)				
REFERENCE	Strausberg, R. Direct Submission Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	QY	1	MetGluAspLeuAspGlnSerProLeuValSerSerSerSerProProArgProGln	20
AUTHORS		Db	187	ATGGAAGACCTGGACCAAGTCTCTCTGGTCTCTCTCGACAGCCACCCCGCGCAG	246
TITLE		QY	21	ProAlaPheLeuTyrGlnPheValArgGluProGluAspGluGluGluGluGlu	40
JOURNAL		Db	247	CCCGCTTCAAGTACCACTTCGTGGAGGAGCCCGAGGAGGAGGAGGAGGAG	306
REMARK		QY	41	GluGluGluAspGluAspGluLeuGluGluValLeuGluArgLysProAla	60
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	Db	307	GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	366
		QY	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
		Db	367	GCCGGGCTGTCGCGGCCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	426
		QY	81	PheGlyAsnAspPheValProAlaProArgGlyPheLeuProAlaAlaProVal	100
		Db	427	TTCCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	486
		QY	101	AlaProGluArgGlnProSerTyrAspProSerProValSerSerThrValProAlaPro	120
		Db	487	GCCCCGGAGCGGACCGCTCTTGGACCGGAGCCCGGCTGTCTGTCGACCGTGC	546
		QY	121	SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro	140
		Db	547	TCCCCGCTGTCTGTCGCGCGAGTCTCGCCCTCCAAAGCTCCCTGAGGAGCAG	606
		QY	141	AlaArgProProProProProProProProProProProProProProProPro	160
		Db	607	GCCCCGGCTCCCGCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	666
FEATURES	Location/Qualifiers	QY	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgGly	180
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gene	1. .1668 /gene="RTN4" /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X" /db_xref="LocusID:57142" /db_xref="MIM:604475"	QY	181	SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	200
		Db	727	TCCTCGGCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	786
		QY	201	ValPheGlyAlaSerPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal	220
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CDS	/gene="RTN4" /codon_start=1 /product="reticulon 4, isoform B" /protein_id="AAH26788.1" /db_xref="GI:20070662" /db_xref="LocusID:57142" /db_xref="MIM:604475"	QY	221	ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly	240
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		Db	907	GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCT	966
		QY	261	GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal	280
		Db	967	GAAGTGTCTATCTATCTGAGAGTGTGTTCAGAGTACAGTAATCTGCTCTTGGTATGTG	1026
		QY	281	AsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu	300
		Db	1027	AACTGCACGATAAAGAACTCAGGCGCTCTCTTCTAGTTGATGATTAGTTAGTTCTCTG	1086
		QY	301	LysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	320
		Db	1087	AAATTGTCAGTGTTCATGTGGGTATTTACCTATGTGTGGTCTGTTTAAATGGTCTGACA	1146
ORIGIN	Alignment Scores: Pred. No.: 4,37e-67 Length: 1668 Score: 1879.00 Matches: 370 Percent Similarity: 99.20% Conservative: 0 Best Local Similarity: 99.20% Mismatches: 3 Query Match: 98.38% Indels: 0	QY	321	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln	340
		Db	1147	CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATTAACCGCATCAG	1206
		QY	341	AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys	360



LOCUS	BC068991	1728 bp	mRNA	linear	PRI 30-JUN-2004
DEFINITION	Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone IMAGE:4634289), complete cds.				
ACCESSION	BC068991				
VERSION	BC068991.1 GI:46362518				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1728)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zuber, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.B., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1728)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs@mail.nih.gov">cgabs@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@bcgsc.bc.ca">info@bcgsc.bc.ca</a> Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lisea Prabh, Parvaneh Saeedi, JR Santos, Angeliq Schnerch, Ursula Skalska, Duane Smalusz, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 54 Row: c Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782 This clone has the following problem: The cds is short compared to the longest cds in the locus. Location/Qualifiers 1. .1728 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4634289" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH_MGC_16"				
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CDS					
ORIGIN	Alignment Scores: Pred. No.: 4,52e-67 Length: 1728 Score: 1879.00 Matches: 370 Percent Similarity: 99.20% Conservative: 0 Best Local Similarity: 99.20% Mismatches: 3 Query Match: 98.38% Indels: 0 DB: 9 Gaps: 0 US-09-544-776-2 (1-373) x BC068991 (1-1728)				
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QY	161 ProProAlaProAlaAlaProProSerThrProAlaAlaProLysArgGly 180				
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RESULT 10
AF148538
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DEFINITION Homo sapiens reticulon 4b mRNA, complete cds.
ACCESSION AF148538
VERSION AF148538.1 GI:10039552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2235)
Yang, J., Yu, L., Bi, A. D. and Zhao, S. Y.
Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->2p13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
JOURNAL 20237542
MEDLINE 10773680
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REFERENCE 2 (bases 1 to 2235)
Zhou, Y., Yu, L. and Zhao, S. Y.
Direct Submission
AUTHORS
TITLE Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P. R. China
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DEFINITION alternatively spliced.
ACCESSION AY102277
VERSION AY102277.1 GI:26800561
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1 (bases 1 to 2332)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
23376540
MEDLINE
PUBMED 12488097
REFERENCE
2 (bases 1 to 2332)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
3 (bases 1 to 2332)
Van der Putten,H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland

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3'UTR

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DEFINITION AK130812

ACCESSION AK130812

VERSION AK130812.1 GI:34527696

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shichata N., Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S., Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R., Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y., Watanabe M., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T. and Sugano S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1525)

AUTHORS Sugano S. and Suzuki Y.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flcdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

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Percent Similarity:	99.20%	Conservative:	1
Best Local Similarity:	98.93%	Mismatches:	3
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CQ769577

LOCUS

DEFINITION

SEQUENCE 303 from Patent WO2003058021.

ACCESSION CQ769577

linear PAT 04-MAR-2004



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REFERENCE	1 Koenig-Hoffman,K., Kazinski,M., Schaefer,R. and Kesper,B. Novel apoptosis-inducing dna sequences Patent: WO 2003058021-A 303 17-JUL-2003; Xantos Biomedicine AG (DE) Location/Qualifiers
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JOURNAL	
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Dd	236 GAAGAGGAGGACGAGGACGAAGACTTGGAGGAGCTGGAGGTGCTGGAGGAAGCCC 295
Qy	61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyValAspMetAsp 80
Dd	296 GCCGGGCTGTCTGGCGGCCAGTGCACACCCCTGCCCGCGCGCCCTCATGGAC 355
Qy	81 PheGlyAsnAspPheValProAlaProAlaProArgGlyPheLeuProAlaAlaProVal 100
Dd	356 TTCCGAATGACTTCGTGCGCGCGCGCCCGCGGACCCCTGCCCGCGCTCCCCCGTC 415
Qy	101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerTherValProAlaPro 120
Dd	416 GCCCGGAGCGGCGAGCGCTTGGAGACCCGAGCGCGGTGTCTGACCGTCCCGCGCCA 475
Qy	121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140
Dd	476 TCCCGGCTGTCTGCCGAGTGTGCGCCTCCAGCTCCCTGAGGACGAGCGCTCCG 535
Qy	141 AlaArgProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
Dd	536 GCCCGGCTCCCTCTCCCGCGCGAGCGTGGAGCCCGGAGGACCCGTTGGAGCC 595
Qy	161 ProProAlaProAlaProProSerThrProAlaAlaProLysLeuArgGly 180
Dd	596 CCGCCAGCCCGGCTCCCGCGCGCCCTCCACCCCGCGCGCCGCCAAGCGAGGCG 655
Qy	181 SerSerGlySerValValValAspLeuLeuTyrrTroArgApIleLysLeuThrClyVal 200
Dd	656 TCCTCGGCTCAGTGTGTGTACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTG 715
Qy	201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220
Dd	716 GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGCAATTGTGAGCGTA 775
Qy	221 ThrAlaTyrrileAlaLeuAlaLeuSerValThrIleSerProArgIleTyrrLysGly 240

## ORIGIN

Alignment Scores: 1.12e-66 Length: 2052  
Pred. No.: 1871.00 Matches: 368  
Score: 98.93% Conservative: 1  
Percent Similarity: 98.93%  
Best Local Similarity: 98.66% Mismatches: 4  
Query Match: 97.96% Indels: 0  
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x AB015639 (1-2052)

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QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu 40  
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Db 127 CCGCGCTTCAAGTACCAGTTCTGTAGGGAGCCGAGGAGGAGGAGGAGGAG 186  
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QY 41 GluGluGluAspGluAspGluAspLeuGluLeuGluValLeuGluArgLysProAla 60  
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Db 187 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
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QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
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Db 247 GCGGGCTGTCCGGGCCCCAGTGTCCACCGCCCTGCGCGCGCGCCCTGATGGAC 306  
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QY 81 PheGlyAsnAspPheValProProAlaProAlaProArgGlyPheLeuProAlaProVal 100  
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QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140  
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Db 427 TCCCCGCTGTCTGTGCGCGAGTCTCGCCCTCCAGCTCCCTCAGGACGCGCGCTCCG 486  
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QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
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Db 487 GCGCGGCTTCCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546  
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QY 161 ProProAlaProAlaProAlaProSerThrProAlaProLysArgArgGly 180  
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Db 547 CCGCCAGCCCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 606  
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QY 181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200  
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QY 221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly 240  
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Db 787 GTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAACTCT 846  
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QY 261 GluValAlaIleSerGluIleValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280  
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Search completed: August 3, 2005, 23:12:11  
Job time : 4346 secs

Db 967 AAGTTTGCAGTGTTCATGTGGGTATTTACCTATGTGGTGCCTTGTTTAATGGTCTGACA 1026  
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	37.4	1.7	50	3	US-08-860-038-17	Sequence 17, Appl
3	37.4	1.7	50	3	US-09-580-923-17	Sequence 17, Appl
4	35.2	1.6	48	4	US-08-979-608A-36	Sequence 36, Appl
5	35.2	1.6	48	4	US-09-517-849-36	Sequence 36, Appl
6	35.2	1.6	48	4	US-09-616-289-36	Sequence 36, Appl
C 7	31	1.4	39	1	US-08-068-747-9	Sequence 9, Appli
8	28	1.2	45	3	US-08-979-608A-30	Sequence 30, Appl
9	28	1.2	45	4	US-09-517-849-30	Sequence 30, Appl
10	28	1.2	45	4	US-09-616-289-30	Sequence 30, Appl
11	27.6	1.2	45	2	US-08-356-786-13	Sequence 13, Appl
C 12	25.8	1.2	50	4	US-09-513-9990-30835	Sequence 13, Appl
13	25.6	1.1	50	4	US-08-956-171E-2153	Sequence 2153, Ap
14	25.6	1.1	50	4	US-08-781-986A-2153	Sequence 2153, Ap
15	25.2	1.1	30	1	US-08-068-747-4	Sequence 4, Appli
C 16	25.2	1.1	30	3	US-08-589-109A-12	Sequence 12, Appl
17	25.2	1.1	41	1	US-08-113-646A-39	Sequence 39, Appl
C 18	25.2	1.1	42	2	US-08-776-94A-4	Sequence 4, Appli
19	25.2	1.1	44	1	US-08-113-648A-40	Sequence 40, Appl
20	24.8	1.1	36	1	US-08-113-646A-6	Sequence 6, Appli
21	24.6	1.1	50	3	US-09-371-489-4	Sequence 4, Appli
C 22	24.4	1.1	42	1	US-08-068-747-10	Sequence 10, Appl
23	24.4	1.1	50	1	US-08-420-443-1	Sequence 1, Appli
24	24.4	1.1	50	4	US-09-621-976-14715	Sequence 14715, A
25	24.2	1.1	37	1	US-08-113-646A-38	Sequence 38, Appl
C 26	24.2	1.1	40	3	US-09-306-290-12	Sequence 12, Appl
27	24.2	1.1	50	3	US-09-930-181-14	Sequence 14, Appl



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; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-36

Query Match      1.6%; Score 35.2; DB 4; Length 48;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 40; Conservative 0; Mismatches 8; Indels 0

QY      234 GACGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCAGCAGCAAGAC 281
Db       1 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCAGCAGCAGCAC 48

RESULT 7
US-08-068-747-9/c
; Sequence 9, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-9

Query Match      1.4%; Score 31; DB 1; Length 39;
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIORITY INFORMATION:
PRIOR APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..45
OTHER INFORMATION: /note="product
OTHER INFORMATION: protein info:
US-08-356-786-13

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..45
OTHER INFORMATION: /note= "product = "old linker"
OTHER INFORMATION: protein info: old linker"
US-08-356-786-13

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[illegible]

-171E-2153  
e 2153, Application US/08956171E  
NO. 6593114  
ADDITIONAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861

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/
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Mark J. Hyman
/   REGISTRATION NUMBER: 46,789
/   REFERENCE/DOCKET NUMBER: PB248P1
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (240) 314-1224
/   TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 2153:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 50 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: double
/     TOPOLOGY: linear
/   SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-08-956-171E-2153
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Best Local Similarity 69.4%; Pred. No. 8.8e+03;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      617  CCGCGCAGCCCGGCTCCCGCGCGCCCTCCACCGCGCGCGCC 665
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RESULT 14
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/ Sequence 2153, Application US/08781986A
/ Patent No. 6737248
/ GENERAL INFORMATION:
/   APPLICANT: Charles Kunsch
/   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/   NUMBER OF SEQUENCES: 5255
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Human Genome Sciences, Inc.
/     STREET: 9410 Key West Avenue
/     CITY: Rockville
/     STATE: Maryland
/     COUNTRY: USA
/     ZIP: 20850
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/   COMPUTER: HP Vectra 486/33
/   OPERATING SYSTEM: MSDOS version 6.2
/   SOFTWARE: ASCII Text
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/781,986A
/     FILING DATE:
/     CLASSIFICATION: 435
/     PRIOR APPLICATION DATA:
/     APPLICATION NUMBER:
/     FILING DATE:
/   ATTORNEY/AGENT INFORMATION:
/     NAME: Benson, Bob
/     REGISTRATION NUMBER: 30,446
/     REFERENCE/DOCKET NUMBER: PB248PP
/   TELECOMMUNICATION INFORMATION:
/     TELEPHONE: (301) 309-8504
/     TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 2153:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 50 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: double
/     TOPOLOGY: linear
/   US-08-781-986A-2153
      1.1%; Score 25.6; DB 4; Length 50;
Query Match
Best Local Similarity 69.4%; Pred. No. 8.8e+03;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

/
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Mark J. Hyman
/   REGISTRATION NUMBER: 46,789
/   REFERENCE/DOCKET NUMBER: PB248P1
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (240) 314-1224
/   TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 2153:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 50 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: double
/     TOPOLOGY: linear
/   SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-08-956-171E-2153
      1.1%; Score 25.6; DB 4; Length 50;
Query Match
Best Local Similarity 69.4%; Pred. No. 8.8e+03;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      617  CCGCGCAGCCCGGCTCCCGCGCGCCCTCCACCGCGCGCGCC 665
Db      1  CCCCCCTCCCGCTCCCGCNCNCCCCCCCCCCCCCCCCCCCC 49

RESULT 15
US-08-068-747-4
/ Sequence 4, Application US/08068747
/ Patent No. 5695933
/ GENERAL INFORMATION:
/   APPLICANT: Schalling, Martin
/   APPLICANT: Hudson, Thomas J.
/   APPLICANT: Housman, David E.
/   TITLE OF INVENTION: Direct Determination of Expanded
/   TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
/   NUMBER OF SEQUENCES: 11
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
/     STREET: Two Militia Drive
/     CITY: Lexington
/     STATE: Massachusetts
/     COUNTRY: USA
/     ZIP: 02173
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/068,747
/     FILING DATE: 28-MAY-1993
/     CLASSIFICATION: 435
/   ATTORNEY/AGENT INFORMATION:
/     NAME: Granahan, Patricia
/     REGISTRATION NUMBER: 32,227
/     REFERENCE/DOCKET NUMBER: MIT-6141
/   TELECOMMUNICATION INFORMATION:
/     TELEPHONE: 617-861-6240
/     TELEFAX: 617-861-9540
/     INFORMATION FOR SEQ ID NO: 4:
/     SEQUENCE CHARACTERISTICS:
/       LENGTH: 30 base pairs
/       TYPE: nucleic acid
/       STRANDEDNESS: single
/       TOPOLOGY: linear
/     MOLECULE TYPE: other nucleic acid
/     DESCRIPTION: /desc = "Synthetic"
/   US-08-068-747-4
      1.1%; Score 25.2; DB 1; Length 30;
Query Match
Best Local Similarity 90.0%; Pred. No. 8.1e+03;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      1  AGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 30

Search completed: August 4, 2005, 02:56:42
Job time : 378 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: August 3, 2005, 17:13:52 ; Search time 573 Seconds  
(without alignments)  
3853.514 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRKAE 373

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1879	98.4	1122	4	Aaf90325 Human NOG
3	1879	98.4	1216	6	Aba05903 Human RTN
4	1879	98.4	1610	3	Aaz36230 cDNA enco
5	1879	98.4	2235	6	Abv94681 Human pan

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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Aac64406 Human Nog  
Adi62860 Human apo  
Abk90133 DNA enco  
Aak94408 Human ful  
Adi11137 Full leng  
Aad08386 Human sec  
Aab55284 Rat fooc  
Aaz56886 Human MAG  
Aaf90324 Human NOG  
Abk90134 DNA enco  
Abn86601 Human neu  
Ade007886 Human pol  
Adri13965 Human NOG  
Aad94550 Human NOG  
Aas09453 Human cDN  
Acc81048 Human Nog  
Adp13574 Renal cel  
Abv94680 Human pan  
Adg32772 Human DNA  
Adr83534 Human ret  
Aaa23454 cDNA enco  
Aab70449 Human bon  
Abx34563 Human mdd  
Adq16433 Construct  
Adp45571 Rat NogoA  
Aad01173 Rat neuro  
Abn86600 Rat neuro  
Ado07888 Mouse pol  
Aaf32725 Human sec  
Adq16433 Nucleotid  
Aad01174 Bovine neu  
Aai98079 Human neu  
Aaf90323 Human NOG  
Aaa72983 Human NSP  
Aax23695 Human NSP  
Aax04379 Human sec  
Adk14166 Human aut  
Aax97587 Extended  
Adp18854 Human sec  
Aav30920 Human sec

PR 19-JUL-1999; 99GB-00016898.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Michalovich D, Prinjha RK;  
 PI WPI; 2000-182693/16.  
 DR P-PSDB; AAY56969.  
 DR  
 XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.  
 XX  
 PS Claim 5; Page 21-22; 35pp; English.  
 XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein variant  
 XX  
 SQ Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3.01e-75 Length: 1122  
 Score: 1879.00 Matches: 370  
 Percent Similarity: 99.20% Conservative: 0  
 Best Local Similarity: 99.20% Mismatches: 3  
 Query Match: 98.38% Indels: 0  
 DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x AAZ56888 (1-1122)

QY	1	MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProArgProGln	20
DB	1	ATGGAGACCTGGACCAAGTCTCTCTGGTCTCGTCTCGACAGCCACCCCGGCGCAG	60
QY	21	ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu	40
DB	61	CCCGCGTTCAAGTACCAAGTTCGTGGAGGAGCCCGGAGGAGGAGGAGGAG	120
QY	41	GluGluGluAspGluAspGluAspGluGluGluValLeuGluArgLysProAla	60
DB	121	GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	180
QY	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
DB	181	GCCGGGCTGTCCGGGCCCCAGTCCACCGCCCTCGCGCGCGCGCCCTGATGGAC	240
QY	81	PheGlyAsnAspPheValProAlaProAlaProArgGlyPheLeuProAlaProVal	100
DB	241	TTTCGGAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	300
QY	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
DB	301	GCCCCGAGCGGAGCGCTCTGGAGCCCGGAGCCCGGTGTCGACCGCGCGCCCA	360
QY	121	SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro	140
DB	361	TCCCCGCTGTCTGCTCCGCGAGTCTCGCCCTCCAGCTCCCTGAGGACGACGAGCTCCG	420
QY	141	AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
DB	421	GCCCGGCTCTCCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	480
QY	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly	180
DB	481	CCGCCAGCCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	540

QY	181	SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	200
DB	541	TCTCGGGCTCAGTGGTGGTGGACCTCTGTACTGGAGAGACATTAAGAGACTGGAGTG	600
QY	201	ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal	220
DB	601	GTGTTTGGTGCCAGCCTATTCTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTA	660
QY	221	ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGly	240
DB	661	ACAGCTCATTTGCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGT	720
QY	241	ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer	260
DB	721	GTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT	780
QY	261	GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal	280
DB	781	GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATCTCTGCTCTTGGTCATGTG	840
QY	281	AsnCysThrIleLysGluLeuArgGluPheLeuValAspLeuValAspSerLeu	300
DB	841	AACTGCAGATAAAGAACTCAGGCGCCTCTTCTTAGTGTGATTTAGTTGATTTCTCTG	900
QY	301	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	320
DB	901	AGTTTGGAGTGTGATTTGGGTATTTACCTATGTTGGTCTCTTTAATGTCGTGACA	960
QY	321	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln	340
DB	961	CTACTGATTTTGGCTCTCATTTTCACTTCTCTGTTCTCTGTTTATTTATGAACGGCATCAG	1020
QY	341	AlaGlnIleAspHisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLys	360
DB	1021	GCACAGATAGATCATTTATCTAGGACTTGCATAAAGAATGTTAAAGATGCTATGCTATAA	1080
QY	361	IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu	373
DB	1081	ATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA	1119
RESULT 2			
ID	AAF90325	AAF90325 standard; cDNA; 1122 BP.	
XX	AAF90325;		
XX	23-JUL-2001	(first entry)	
DE	Human NOGO-B cDNA.		
XX	NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;		
XX	stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;		
XX	neuromuscular disorder; psychiatric disorder; developmental disorder;		
XX	neuroprotective; nootropic; neuroleptic; antiparkinsonian;		
XX	cerebroprotective; neuroleptic; diagnosis; therapy; ss.		
OS	Homo sapiens.		
XX	WO200136631-A1.		
XX	25-MAY-2001.		
XX	14-NOV-2000; 2000WO-GB004345.		
XX	15-NOV-1999; 99GB-00026995.		
XX	24-JAN-2000; 2000GB-00001550.		
XX	(SMIK ) SMITHKLINE BEECHAM PLC.		
XX	Michalovich D, Prinjha R;		
XX	WPI; 2001-343822/36.		
XX	P-PSDB; AAB82350.		

XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 27; 25pp; English.

XX The present sequence is that of cDNA encoding human NOGO-B (see  
CC AAB82350). NOGO-B is a previously known splice variant of the human NOGO  
CC gene on chromosome 2p21. The invention relates to a novel NOGO gene  
CC splice variant, NOGO-C (see AAF90325). It provides NOGO-C polypeptides  
CC and polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and antagonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels

XX SQ Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 3,01e-75 Length: 1122  
Score: 1879.00 Matches: 370  
Percent Similarity: 99.20% Conservative: 0  
Best Local Similarity: 99.20% Mismatches: 3  
Query Match: 98.38% Indels: 0  
DB: 4 Gaps: 0

US-09-544-776-2 (1-373) x AAF90325 (1-1122)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20  
DB 1 ATCGAAGACCTGGACACCATCTCTCTGTCGTCTCGGACAGCCACCCCGCGCGAG 60  
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
DB 61 CCCGCGTTCAAGTACCAGTTCTGTGAGGAGCCCGGAGCAGGAGGAGNAGAGGAGGAG 120  
QY 41 GluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGluGluGlu 60  
DB 121 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
DB 181 GCCGGGCTGTCCGGGCGCCCGAGTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 240  
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaProProVal 100  
DB 241 TTGCGAAATGACTTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120  
DB 301 GCCCGGAGCGGAGCGGCTCTTGAGACCCGAGCGCGGTGCTGCGACCGTCCCGGCCA 360  
QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro 140  
DB 361 TCCCGCGTGTCTGTCGCGCAGTCTCGCCCTCCCAAGCTCCCTGAGCAGCAGCCTCCG 420  
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
DB 421 GCCCGGCTCTCCCTCTCCCGGCGCAGGTGAGCCCCCAGGAGCCCGTGTGAGCC 480  
QY 161 ProProAlaProAlaProAlaProProSerThrProAlaProLysArgArgGly 180  
DB 481 CCGCCAGCCCGGCTCCCGCGCGCGCCCTCCACCCCGCGCCCGCCCAAGCGCAGGGC 540  
QY 181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysThrGlyVal 200  
DB 541 TCCTCGGGCTCAGTGGTGTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGT 600

QY 201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220  
DB 601 GTGTTTGGTGGCCAGCCTATTCTCTGCTGCTTTCATTGACAGATTTCAGCATTTGTGAGCGTA 660  
QY 221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly 240  
DB 661 ACAGCCTACATTGCTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGT 720  
QY 241 ValIleGluAlaTleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260  
DB 721 GTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGGCATATCTGGAATCT 780  
QY 261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280  
DB 781 GAAGTTGCTATATCTCAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTG 840  
QY 281 AsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu 300  
DB 841 AACTGCAGATAAAGGAACCTCAGGCGCCTCTCTTAGTTGATGATTAGTTGATTCTCTG 900  
QY 301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320  
DB 901 AGTTTGCAGTGTGTGATGTGGGTATTACCTATGTTGGTCCCTTGTTTAAATGTTCTGACA 960  
QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340  
DB 961 CTACTGATTTGGCT 1020  
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360  
DB 1021 GCACAGATAGATCATTTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAA 1080  
QY 361 IleGlnAlaLysTleProGlyLeuLysArgLysAlaGlu 373  
DB 1081 ATCCAAGCAAAATCCCTGATTTGAAGCGCAAGCTGAA 1119  
RESULT 3  
ABA05903  
ID ABA05903 standard; cDNA; 1216 BP.  
XX ABA05903;  
AC ABA05903;  
XX  
DT 04-MAR-2002 (first entry)  
XX  
DE Human RTN4B encoding cDNA SEQ ID NO 3.  
XX  
KW Human; RTN4B; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 5..1126  
FT /\*tag= a  
FT /product= "RTN4B"  
XX  
XX CN1311439-A.  
XX  
XX PD 05-SEP-2001.  
XX  
XX PF 02-MAR-2000; 2000CN-00111791.  
XX  
XX PR 02-MAR-2000; 2000CN-00111791.  
XX  
XX (UYFU-) UNIV FUDAN.  
XX  
XX Yu L, Fu Q, Zhao Y;  
PI WPI; 2002-049934/07.  
XX  
XX P-PSDB; AAM47954.  
XX  
XX Human RTN 4B protein and coding sequence, its preparation and use.  
XX



[illegible]

PA (CORI-) CORIXA CORP.  
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX WPI; 2002-627435/67.  
 DR P-PSDB; ABP68601.  
 XX  
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
 PT cancer.  
 XX  
 PS Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV94145); (b)  
 CC complements of (a); (c) sequences consisting of at least 20 contiguous  
 CC residues of (a); (d) sequences that hybridize to (a), under moderately  
 CC stringent conditions; (e) sequences having at least 75% or 90% identity  
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
 CC in a patient and compositions comprising polypeptides, polynucleotides,  
 CC antibodies, fusion proteins, T cell populations and antigen presenting  
 CC cells expressing the polypeptide are useful in treating pancreatic cancer  
 CC and stimulating an immune response. The polynucleotides can be used as  
 CC probes or primers for nucleic acid hybridisation, in the design and  
 CC preparation of ribozyme molecules for inhibiting expression of the tumour  
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
 CC therapy. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 5.59e-75 Length: 2235  
 Score: 1879.00 Matches: 370  
 Percent Similarity: 99.20% Conservative: 0  
 Best Local Similarity: 99.20% Mismatches: 3  
 Query Match: 98.38% Indels: 0  
 DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x ABV94681 (1-2235)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20  
 DB 142 ATGGAGAGCTGGACGACGCTCTCTGGTCTCTCTGGACAGCCACCCCGCGCGAG 201  
 QY 21 ProAlaPheLysTyrglnPheValArgGluProGluAspGluGluGluGluGlu 40  
 DB 202 CCGCGTTCAAGTACCAGTTCTGGAGGAGCCCGAGGACGAGGAGGAGGAGGAG 261  
 QY 41 GluGluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGlu 60  
 DB 262 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 321  
 QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
 DB 322 GCCGGGCTGTCGGGGCCCCAGTGGCCCGCCCTGCGCGCGCGCGCGCGCGCGCG 381  
 QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProVal 100  
 DB 382 TTCGGAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTC 441  
 QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120  
 DB 442 GCCCGGAGCGGAGCGGCTTTGGGACCGGAGCGGCTGCTGCGACCGCGCGCGCA 501  
 QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluProPro 140  
 DB 502 TCCCGCTGTCTGTCGCGCGAGTCTCGCCCTCCAGCTCCCTGAGGACGAGGCTCGG 561  
 QY 141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160

DB 562 GCCCGGCTCCCTCTCCCGCGCAGCGGTGAGCCGCCCGCAGAGCCCGTGTGGACC 621  
 QY 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly 180  
 DB 622 CCGCCAGGCCCCGCTCCCGCGCGCGCCCTCCACCGCGCGCGCCCAAGCGCAGGGC 681  
 QY 181 SerSerGlySerValValValValValValValValValValValValValValVal 200  
 DB 682 TCCTCGGGCTCAGTGGTGTGGTCCCTCTGTTACTGAGAGCATTAAGAAGACTGGAGTG 741  
 QY 201 ValPheGlyAlaSerPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 220  
 DB 742 GTGTTTGGTGGCAGCCTATTCTCTGCTTTCATTGACAGTATTTCAGCATTTGAGCGTA 801  
 QY 221 ThrAlaTyrlleAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 240  
 DB 802 ACAGCTCATTTGGCTTGGCCCTCTCTGTGTGACCATCAGCTTTAGGATATACAAAGGT 861  
 QY 241 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrlleuGluSer 260  
 DB 862 GTGATCCAGCTATTCAGANATCAGATGAGGCCACCCATTCAGGGCATATCTGGAATCT 921  
 QY 261 GluValAlaileSerGluGluLeuValGlnLysTyrlleSerAsnSerAlaAlaGlyHisVal 280  
 DB 922 GAAATTGCTATATCTGAGGAGTTGGTTTCAAGAGTACAGTAATTTCTGCTCTTGGTCATGTG 981  
 QY 281 AsnCysThrileGlyGluLeuArgLeuPheLeuValAspLeuValAspSerLeu 300  
 DB 982 AACTCCAGATTAAGAACTCAGGCGCTCTCTTTAGTTGATGATTTAGTTAGTTCTCTG 1041  
 QY 301 LysPheAlaValLeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThr 320  
 DB 1042 AGTTTGGAGTGTGATGTTGGTATTTACCTATGTTGGTCTGCTTTTAATGCTGTACA 1101  
 QY 321 LeuLeuileLeuAlaLeuileSerLeuPheSerValProValileTyrgluArgHisGln 340  
 DB 1102 CTACTGATTTTGGCTCTCATTTCACTTCACTGTTCTCTGTTTATTTATGACCGCATCAG 1161  
 QY 341 AlaGlnileAspHisTyrlleuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLys 360  
 DB 1162 GCACAGATAGATCATTTATCTAGGACTTGCANATAAGAATGTTAAAGATGCTATGCTAAA 1221  
 QY 361 ileGlnAlaLysileProGlyLeuLysArgLysAlaGlu 373  
 DB 1222 ATCCAGCAGCAAAATCCCTGGATTGAGGCGCAAGCTGHA 1260  
 RESULT 6  
 AAC64406  
 ID AAC64406 standard; cDNA; 2240 BP.  
 XX AAC64406;  
 AC AAC64406;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human Nogo B nucleotide sequence SEQ ID NO:1.  
 XX  
 KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;  
 KW stress-phosphorylated endoplasmic reticulum protein; cytostatic;  
 KW gene therapy; cell growth; cellular stress response; neuron growth;  
 KW regulator of oxidative stress; inhibitor of neurite outgrowth;  
 KW axon regeneration; diagnosis; cancer; identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200060083-A1.  
 PN  
 XX  
 PD 12-OCT-2000.  
 XX  
 XX 07-APR-2000; 2000WO-US009383.  
 PF  
 XX  
 PR 08-APR-1999; 99US-0128372P.  
 PR 21-JUN-1999; 99US-0140331P.  
 XX











PR 02-MAY-2000; 2000JP-00183865.  
 PR 07-JUL-2000; 2000EP-00114089.  
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2004-204755/20.  
 DR P-PSDB; ADL31138.  
 XX  
 XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
 PT length human cDNAs.  
 XX  
 XX Example 1; SEQ ID NO 3170; 1340pp; English.  
 XX  
 XX This invention relates to a novel primers useful for synthesizing full  
 CC length cDNA molecules that encode human proteins. Specifically, it refers  
 CC to secretory or membrane proteins that are potential therapeutic agents/  
 CC target molecules in the field of medicine, and in particular genes  
 CC encoding proteins that are associated with signal transduction,  
 CC glycoproteins and transcription. The present invention describes a method  
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
 CC ends using the oligo-capping method. This polynucleotide sequence is a  
 CC full length human cDNA clone of the invention.  
 XX  
 XX Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2.48e-74 Length: 1694  
 Score: 1862.00 Matches: 369  
 Percent Similarity: 98.66% Conservative: 0  
 Best Local Similarity: 98.66% Mismatches: 4  
 Query Match: 97.49% Indels: 1  
 DB: 12 Gaps: 0

US-09-544-776-2 (1-373) x ADL31137 (1-1694)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20  
 DB 232 ATGGAGACCTGGACCACTCTCTCTGCTCTGCTCTGGACAGCCACCCCGCGCGCAG 291  
 QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
 DB 292 CCGCGCTTCAAGTACCAAGTTCGTGAGGAGCCCGGAGGAGGAGGAGGAGGAG 351  
 QY 41 GluGluGluAspGluAspGluGluGluGluGluGluGluGluGluGluGluGlu 60  
 DB 352 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 411  
 QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
 DB 412 GCGGGCTGTCCGGGCCCCAGTGCCACCGCCCTGCGCCGGGCGGCCCTGTATGGAC 471  
 QY 81 PheGlyAsnAspPheValProProAlaProAlaProArgGlyPheLeuProAlaProVal 100  
 DB 472 TTCGAAATGACTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTT 531  
 QY 101 -AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPr 120  
 DB 532 CGCCCCGAGGAGGAGCGCGCTTGGGACCCGAGCGCGGTCGTGCGAGCGCGCGCGCC 591  
 QY 120 oSerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPr 140  
 DB 592 ATCCCGCTGTCTGCTGCCGAGTCTCGCCCTCCAGCTCCCTGAGGAGGAGGAGGAGGAG 651  
 QY 140 oAlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpTh 160  
 DB 652 GGGCGGCGCTCCCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 711  
 QY 160 rProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgGlu 180  
 DB 712 CCGGCCAGCCCGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGG 771

QY 180 YSerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVa 200  
 DB 772 CTCTCGGGCTCAGTGGTGTGGACCTCTGTACTGGAGAGACATTAAGAAGAGCTGAGT 831  
 QY 200 lValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVa 220  
 DB 832 GGTGTGGTGTGCTGCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATGTCAGCGT 891  
 QY 220 lThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGl 240  
 DB 892 AACAGCTCATTCCTGCTGCTCTCTGTGACCATCAGCTTTCAGGATATACAGGG 951  
 QY 240 YValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 260  
 DB 952 TGTGATCCAGCTATCCAGAAATCAGATGAAGCCACCCATTTCAGGGCATATCTGGAATC 1011  
 QY 260 rGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVa 280  
 DB 1012 TGAAGTTGCTATATCTGAGGAGTGGTTCAGAAAGTACAGTAATTCCTGCTCATGT 1071  
 QY 280 lAsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLe 300  
 DB 1072 GAATGACAGTAAAGAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCT 1131  
 QY 300 uLysPheAlaValLeuMetTrpValPheThrTyrValGlyValAlaLeuPheGlnGlyLeuTh 320  
 DB 1132 GAAGTTTGAGTGTGATGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGCTGTAC 1191  
 QY 320 rLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGl 340  
 DB 1192 ACTACTGATTTGGCTCTCATTTCACTTTCAGTGTTCCTGTTTATTTATGAACGGCATCA 1251  
 QY 340 nAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLy 360  
 DB 1252 GGCACAGATAGATCATTTCTAGGACTTGCAGATTAAGATGTTAAGATGCTATGGCTAA 1311  
 QY 360 sIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373  
 DB 1312 AATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 1351

RESULT 11  
 AD08386  
 ID AAD08386 standard; cDNA; 1683 BP.  
 XX  
 AC AAD08386;  
 XX  
 DT 09-AUG-2001 (first entry)  
 XX  
 DE Human secreted protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52.  
 DE  
 KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnerability; cell culture;  
 KW chemotaxis; food additive; gene therapy; binding partner identification;  
 KW ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 CDS 830..1192  
 FT /tag= a  
 FT /product= "Human secreted protein precursor"  
 FT /note= "CDS does not include start codon"  
 FT /partial  
 FT sig\_peptide  
 FT 830..898  
 FT /\*tag= b

FT mat\_peptide 899. .1189  
 PT /\*tag= c  
 PT /product= "Mature human secreted protein"  
 XX  
 PN WO200077022-A1.  
 XX  
 PD 21-DEC-2000.  
 XX  
 XX 01-JUN-2000; 2000WO-US015136.  
 PF  
 XX 11-JUN-1999; 99US-0138629P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Ruben SM, Komatsoulis GA;  
 PI WPI; 2001-367020/38.  
 XX P-PsDB; AAE03939.  
 DR  
 XX  
 XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
 PT disease, botulism, cancers and Schmitar syndrome.  
 PT  
 XX Claim 1; Page 520; 614pp; English.  
 PS  
 XX  
 CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
 CC protein genes and AAE03938-AAE03947 represent the proteins they encode.  
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.  
 CC The genes and their secreted proteins are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 50 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g. rheumatoid arthritis), inflammation, allergies, disease,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC angiotensin-related disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infectious. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The  
 CC present sequence represents a human secreted protein-encoding cDNA of the  
 CC invention  
 XX  
 XX Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3,45e-68 Length: 1683  
 Score: 1723.50 Matches: 346  
 Percent Similarity: 92.76% Conservative: 0  
 Best Local Similarity: 92.76% Mismatches: 4  
 Query Match: 90.24% Indels: 24  
 DB: 4 Gaps: 1  
 US-09-544-776-2 (1-373) x AAD08386 (1-1683)  
 QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProArgProGln 20  
 DB 233 ATGGAGAGCTGGACCAAGTCTCTCTGGTCTCTGGACAGCCACCCTGGCCGCGCAG 292  
 QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu 40  
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Db 293 CCCGGCTTCAAGTACCAGTTCTGAGGGAGCCGAGGACGAGGAGAGGAGGAG 352  
 QY 41 GluGluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGlu 60  
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 Db 353 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 412  
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 QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
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 Db 413 GCGGGGCTGTGCGGGGCCAGTGCACCGCCCTGCGCGCGCGCGCGCGCGCGCGCG 472  
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 QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProVal 100  
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 Db 473 TTTCGGAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTC 532  
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 QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerTrpValProAlaPro 120  
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 Db 533 GCGCGGAGCGGCGCGCGCTTGGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCA 592  
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 QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 593 TCCCGCTGTCTGCTGCGCGAGTCTCGCCCTCCAGCTCCCTGAGGACGAGCGCTCCG 652  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
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 Db 653 GCGCGCGCTCCCGCTCTCTCCCGCGCGCGCGTGGCGCGCGCGCGCGCGCGCG 712  
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 QY 161 ProProAlaProAlaProAlaProProSerTrpProAlaProLysArgArgGly 180  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 713 CCGCGAGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 772  
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 QY 181 SerSerGlySerValValValAspLeuLeuTrpArgAspLysLysLysThrGlyVal 200  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 773 TCCTGGGCTCAGTGGTGTGTGACCTCTCTGTAAGGAGACATTAAGAGGACTGGAGTG 832  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 201 ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 220  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 833 GGTGTTGGTGGCGAGCTATTCTCTGCTCTTTCATTCAGCATTTTCAGCATTTG 892  
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 QY 221 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGly 240  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 893 ACAGCTCATATGCTTGGCGCTCTCTCTGTAAGGAGACATTAAGAGGACTGGAGTG 952  
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 QY 241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 953 GTGATCCAGCTATCCAGAAATCAGATGAAGCGCCACCCATTTCAGGCAATCTCTGAATCT 1012  
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 QY 261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1013 GAAGTTGCTATATCTCAGGAGTGGTTCAGAAAGTACAGTAATCTCTCTCTGTCATGTG 1072  
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 QY 281 AsnCysThrIleLysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeu 300  
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 Db 1073 AACTGCAGATAAAGAACTCAGGCGCTCTCTCTTAGTGTGATGATTTAGTGTCTCTG 1132  
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 QY 301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320  
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 Db 1133 AAGCT----- 1137  
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 QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340  
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 Db 1138 -----CTCATTTTCACTCTTTCACTGTGTTCTCTGTTTATTTATGAACGCGCATCAG 1182  
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 QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360  
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 Db 1183 GCACAGATAGATCATTTATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGCTATAA 1242  
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 QY 361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373  
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 Db 1243 ATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 1281  
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 RESULT 12  
 ADB85284  
 ID ADB85284 standard; DNA; 2782 BP.



XX AAZ56886;  
 AC  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 XX Human MAGI polypeptide encoding DNA.  
 DE  
 XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1. .3579  
 FT CDS  
 FT /\*tag= a  
 FT /product= "MAGI polypeptide"  
 XX  
 XX WO200005364-A1.  
 PN  
 XX  
 PD 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-GB002360.  
 XX  
 XX 22-JUL-1998; 98GB-00016024.  
 PR 19-JUL-1999; 99GB-00016898.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA  
 XX Michalovich D, Prinjha RK;  
 PI  
 XX WPI; 2000-182693/16.  
 DR P-PSDB; AAY56967.  
 DR  
 XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.  
 PT  
 XX Claim 5; Page 19-20; 35pp; English.  
 PS  
 XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein  
 CC  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.53e-56 Length: 3579  
 Score: 1459.50 Matches: 370  
 Percent Similarity: 31.04% Conservative: 0  
 Best Local Similarity: 31.04% Mismatches: 3  
 Query Match: 76.41% Indels: 819  
 DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x AAZ56886 (1-3579)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20  
 DB 1 ATGGAAGACCTGGACCAAGTCTCTCTGGTCTCGTCTCGACAGCCACCCGGCGCAG 60  
 QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu 40  
 DB 61 CCGCGCTTCAAGTACCAGTTCTGTAGGGAGCCCGCAGCAGGAGGAGGAGGAG 120  
 QY 41 GluGluGluAspGluAspGluAspGluGluGluValLeuGluArgLysProAla 60  
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DB 121 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTCTGAGAGGAAGCCCGCC 180  
 QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaAlaGlyAlaProLeuMetAsp 80  
 DB 181 GCCGGGCTGTCCGGCGGCCCCAGTGCACCCGCTCGCGCGCGCGCCCTGTATGAGAC 240  
 QY 81 PheGlyAsnAspPheValProProAlaProAlaProAlaPheLeuProAlaAlaProProVal 100  
 DB 241 TTCGGAATAGATTCTGTCCCGCGCGCGCCCGGAGACCCCTGCCGCGCTCCCGCCGTC 300  
 QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120  
 DB 301 GCCCGGAGCGGCGAGCGTCTTGGGACCCGAGCCCGGTGCTGCGACCGTGCCTGCCCA 360  
 QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluProPro 140  
 DB 361 TCCCGCTGTCTGTGCGCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACACAGAGCTCCG 420  
 QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
 DB 421 GCCCGGCTCCCTCTCTCCCGCGCAGCGTGAGCCCGCCAGGACAGCCGTGTGGACC 480  
 QY 161 ProProAlaProAlaAlaProProSerThrProAlaAlaProLysArgGly 180  
 DB 481 CGCCAGCCCGGCTCCCGCGCGCCCTCCACCCCGCGCGCCCAAGCGCAGGGGC 540  
 QY 181 SerSerGlySerVal----- 185  
 DB 541 TCCTCGGCTCAGTGGATGAGACCCCTTTTGTCTTCTGCTGTCATCTGAGCCTGTGATA 600  
 QY 185 ----- 185  
 DB 601 CGCTCCTGCGAGAAATATGGAATTGAAGGAGCAGCAGGTAAACACTATTTCCGGTGT 660  
 QY 185 ----- 185  
 DB 661 CAAGAGGATTTCCCATCTGCTGCTTGAACTGCTGCTTCTTCTTCTTCTCTGCTCTC 720  
 QY 185 ----- 185  
 DB 721 CTCTCAGCGCTTCTTTCAAAGAAATGAATACCTTGGTAATTTGTCAACATATTACCC 780  
 QY 185 ----- 185  
 DB 781 ACTGAAGNACACTTCAAGAAATGTCAGTGAAGCTTCTAAAGAGTCTCAGAGAAGGCA 840  
 QY 185 ----- 185  
 DB 841 AAAACTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAAATCTCAGAAATG 900  
 QY 185 ----- 185  
 DB 901 GGATCATCGTTGAGTGTCTCTCAAAGCAGAAATCTGCGTAAATAGTAGCAAAATCTTAG 960  
 QY 185 ----- 185  
 DB 961 GAAGAAATAATCGTGAATAATAAGATGAGAGAGAGTGTAGTAGTAATACATCCTT 1020  
 QY 185 ----- 185  
 DB 1021 CATAATCAACAGAGTTACTACAGCTCTTACTAAATTGTTTAAAGAGGATGAAGTTGTG 1080  
 QY 185 ----- 185  
 DB 1081 TCTTCAGAAAAAGCAAAAGACAGTTTTAAATAAGAGAGGTTGCAGTGAAGCTCTATG 1140  
 QY 185 ----- 185  
 DB 1141 AGGAGGAATATGAGACTTCAACCACTTTGAGCGAGTATGGAAAGTGAAGATAGTAAG 1200  
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 DB 1201 GAAGATAGTATATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAACTTGGAAAGATAAGTG 1260

QY 185 ----- 185  
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Db 1321 AGTAATGATGATACTTCTCTTTCCAGTACGCCGAGAAGGTATAAAGGATCGTCCAGGAGCA 1380  
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QY 185 ----- 185  
Db 1441 CCTTTGTTAGGAGATCCTACTTCAGAAAAAAGACCGATGAAAAAATAAGAGAAAG 1500  
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Db 1621 GAAGTCGTGCAAAACATGCTGGAAGGCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680  
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Db 1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAAAAATAATGGACTTGGTT 1740  
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Db 1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCTCTGCACGACAGCTTTGGCCCATCATTT 1800  
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Db 1801 GAAGAGTCAGAAGCTACTCTTCACCAGTTTTCCTGACATTGTTATGGAAGCACCATTG 1860  
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Db 2221 GATTCTGAACCAAGTTGATTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAAACAA 2280  
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Db 2281 GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA 2340

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Db 2341 GAATATGAAAAATAAGAAAAAACTCAGTGTCTTCCACCTGAGGAGGAAAGCCATATTTG 2400  
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Db 2581 GATTCAATCTCCAATTGAAATTTATAGATGAGTTCCCTACATTTGATCAGTTCTAAAACTGAT 2640  
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Db 2641 TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAATATCCACAAAAAGTGAAATT 2700  
QY 185 ----- 185  
Db 2701 GCTAATGCCCCGATGGAGCTGGGTCAATTGCTTGCACAGAAATGGCCCATGACCTTTCT 2760  
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Db 2821 AATGGGTCTGCTACATCAAAAGGTGCTCTTATTTGCCCTCCAGATGTTTCTGCTTTGGCCACT 2880  
QY 185 ----- 185  
Db 2881 CAAGCAGAGATAGAGCATAGTTAAACCCAAAGTTCTTGTGAAGAAGCTGAGAAAAAA 2940  
QY 185 ----- 185  
Db 2941 CTTCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGTATATTTTCAGCAGAGCTG 3000  
QY 186 ----- ValValAspLeuLeuTyrTrpArgAspIleIleValysIleValVal 201  
Db 3001 AGTAAAACTTCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAGAAGACTGGAGTGGTG 3060  
QY 202 PheGlyAlaSerLeuPheLeuSerLeuThrValPheSerIleValSerValThr 221  
Db 3061 TTTGGTGCAGCCTATTCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACA 3120  
QY 222 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrIleVal 241  
Db 3121 GCTCATTTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTG 3180  
QY 242 IleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 261  
Db 3181 ATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAA 3240  
QY 262 ValAlaIleSerGluIleValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsn 281  
Db 3241 GTTGTCTATATCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCATGTGAAC 3300  
QY 282 CysThrIleIleGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIle 301  
Db 3301 TGCACGATAAAGAACTCAGGCGCTCTTCTTAGTTGATGATTAGTTGATTTCTCTGAAG 3360  
QY 302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321  
Db 3361 TTTGTCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTA 3420  
QY 322 LeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 341

Db 3421 CTGATTTGGCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCG 3480  
QY 342 GlnIleAspHisTyrIleuGlyIleuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 361  
Db 3481 CAGATAGATCATTTATCTAGGACTTGCATAATAAGAAATGTTAAAGATGCTATGCTGCTAAATC 3540  
QY 362 GlnAlaLysIleProGlyIleuLysArgLysAlaGlu 373  
Db 3541 CAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 14  
AAF90324  
ID AAF90324 standard; cDNA; 3579 BP.  
XX  
AC AAF90324;  
DT 23-JUL-2001 (first entry)  
XX Human NOGO-A cDNA.  
XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
XX Homo sapiens.  
OS  
XX WO200136631-A1.  
XX  
XX 25-MAY-2001.  
XX  
XX 14-NOV-2000; 2000WO-GB004345.  
XX  
XX 15-NOV-1999; 99GB-00026995.  
PR 24-JAN-2000; 2000GB-00001550.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX Michalovich D, Prinjha R;  
PI  
XX WPI; 2001-343822/36.  
DR P-PSDB; AAB82349.  
XX  
XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.  
XX  
XX Disclosure; Page 25-26; 25pp; English.  
XX  
XX The present sequence is that of cDNA encoding human NOGO-A (see  
CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO  
CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of  
CC human spinal cord cDNA. The invention relates to a novel splice variant,  
CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and  
CC polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and antagonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels  
XX  
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 353e-56 Length: 3579  
Score: 1459.50 Matches: 370  
Percent Similarity: 31.04% Conservative: 0

Best Local Similarity: 31.04% Mismatches: 3  
Query Match: 76.41% Indels: 819  
DB: 4 Gaps: 1  
US-09-544-776-2 (1-373) x AAF90324 (1-3579)  
QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerSerSerProProArgProGln 20  
Db 1 ATGGAAGACCTGGACCACTCTCTGGTCTCGTCTCGACAGCCACCCCGGCGCAG 60  
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
Db 61 CCGCGTTCAAGTACCAGTTCTGTGAGGAGCCGAGGACGAGGAGGAGGAG 120  
QY 41 GluGluGluAspGluAspGluAspLeuGluGluGluGluValLeuGluArgLysProAla 60  
Db 121 GAAGAGGAGGACGAGGACGAGACCTGGAGGAGCTGGAGGTCTGGAGAGGAGCCGCC 180  
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyValProLeuMetAsp 80  
Db 181 GCCGGCTGTCCGCGGCCCGCCAGTGCACCCCTGCCGCGCGCGCCCTGATGAC 240  
QY 81 PheGlyAsnAspPheValProProAlaProAlaProArgGlyPheLeuProAlaAlaProVal 100  
Db 241 TTCGGAATGACTTCTGCGCGCGCGCGCGCGGAGCCCTGCCGCGCGCTCCCCCGTC 300  
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120  
Db 301 GCCCGGAGCGGCGCGCTTGGGACCGCGCGGTCTCGTCCGTCGCGCGCGCA 360  
QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140  
Db 361 TCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAGCTCCCTGAGGACGACGAGCTCCG 420  
QY 141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
Db 421 GCCCGCTTCCGCTCTCCCGCGCGAGCGTGAGCCCGCGCGCGCGCGCGCGCGCG 480  
QY 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgGly 180  
Db 481 CCGCAGCCCGCGCTCCCGCGCGCGCTCCACCCCGCGCGCGCGCGCGCGCGCGCG 540  
QY 181 SerSerGlySerVal----- 185  
Db 541 TCTCGGCTCAGTGGATGAGACCCCTTTTGTCTCTCTGCTGCTGCTGAGCTGTGATA 600  
QY 185 ----- 185  
Db 601 CGCTCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTTCGGCTGGT 660  
QY 185 ----- 185  
Db 661 CAAGAGGATTTCCCATCTGTCTGTTGAACTGCTGTTCTTCTTCTTCTTCTTCTCTCT 720  
QY 185 ----- 185  
Db 721 CTCTCAGCGCTTCTTCAAGAACATGATACCTTGGTAATTTGTCAACAGTATTACCC 780  
QY 185 ----- 185  
Db 781 ACTGAAGGAACACTTCAAGAAAATGTAGTGAAGCTTCTTAAAGAGGTCTCAGAGAAGCA 840  
QY 185 ----- 185  
Db 841 AAACTCTACTCATAGATAGATTTAACAGAGTTTTCAGAAATTAGATCTCAGAAATG 900  
QY 185 ----- 185  
Db 901 GGATCATCTTCAGTGTCTCTCCAAAAGCAGAACTCTGCCGTAATAGTAGCAATCTTAGG 960  
QY 185 ----- 185  
Db 961 GAAGAAATAATCGTGAAAAATAAAGATGAAGAGAGAAGTTAGTTAGTAATAACATCCTT 1020



QY	185	-----	185	QY	185	-----	185
Db	1021	CATAATCAACAGATTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTTG	1080	Db	2101	TTAATTAAGAAACAAAGCTTTCTGCTGAACAGCTCCGGATTTCTCTGATTATTAGAA	2160
QY	185	-----	185	QY	185	-----	185
Db	1081	TCCTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGAAGCTCCTATG	1140	Db	2161	ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTTGAAGATTCTCACCT	2220
QY	185	-----	185	QY	185	-----	185
Db	1141	AGGAGGAATATGCAGACTTCAAAACCATTTGAGCGAGTATGGGAAGTGAAGATAGTAAG	1200	Db	2221	GATTCGACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAACAA	2280
QY	185	-----	185	QY	185	-----	185
Db	1201	GAAGATAGTATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTGGAAAGTAAAGTG	1260	Db	2281	GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCAITTTGAGTCAATGATA	2340
QY	185	-----	185	QY	185	-----	185
Db	1261	GATAAAAAATGTTTTGCAGATAGCCTTTGCCAGTACGCCAAGGTATAAAGGATCGTCAGGAGCA	1320	Db	2341	GAATATGAATAAAGGAAAAACTCAGTGTCTTGGCCACTGAGGAGGAAAGCCATATTTG	2400
QY	185	-----	185	QY	185	-----	185
Db	1321	AGTAATGATGATACTTCTTTCCCGAGTACGCCAAGGTATAAAGGATCGTCAGGAGCA	1380	Db	2401	GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTCTGATGAAGTTTCA	2460
QY	185	-----	185	QY	185	-----	185
Db	1381	TATATCACATGTGCTCCCTTTAACCAGCAGCAACTCGAGGACATTGCAACAAACATTTTT	1440	Db	2461	ACATTGAGCAAAAAGGAGAAAATTCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT	2520
QY	185	-----	185	QY	185	-----	185
Db	1441	CTTTGTTAGGAGATCCTACTTCAGAAAAATAGACCGATGAAAAAAAATAGAAAGAAAG	1500	Db	2521	TCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA	2580
QY	185	-----	185	QY	185	-----	185
Db	1501	AGGCCCAATAGTAACAGAGAAGATACTAGCACCAAAACATCAAAACCCCTTTCTTGTA	1560	Db	2581	GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAACATGAT	2640
QY	185	-----	185	QY	185	-----	185
Db	1561	GCAGCACAGGATTCGAGACAGATTATGTCAACAACAGATAATTTAACAAGGTGACTGAG	1620	Db	2641	TCATTTTCTAAATTAGCCAGGGAATATAGTACCTAGAGATATCCCAACAAAGTGAATTT	2700
QY	185	-----	185	QY	185	-----	185
Db	1621	GAAGTCGTGCAACATGCCTGAAGCCTGACTCCAGATTAGTACAGGAAGCATGTGA	1680	Db	2701	GCTAATGCCCCGATGGAGCTGGTCAITTCGCTTGCACAGAAATGGCCCATGACCTTTCT	2760
QY	185	-----	185	QY	185	-----	185
Db	1681	AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAAACAAAATGGACTTGGTT	1740	Db	2761	TTGAAGAACATACAAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTCTAAA	2820
QY	185	-----	185	QY	185	-----	185
Db	1741	CAAAATCAGAACTTATGCAAGAGTCACTCTATCCTGCAGACAGCTTTGCCCATCATTT	1800	Db	2821	AATGGGTCTGTACATACAAAGGTGCTTTATTGTCCTCCAGATGTTTCTGCTTTGGCCACT	2880
QY	185	-----	185	QY	185	-----	185
Db	1801	GAAGAGTCAGAGCTACTCCTTACCAGTTTTGCTGACATTTGTATGGAAGCACCATTG	1860	Db	2881	CAAGCAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAGAGAGCTGAGAAAAA	2940
QY	185	-----	185	QY	185	-----	185
Db	1861	AATTCTGCAGTTCTAGTGTGCTGCTTCCGTGATACAGCCAGCTCATCAACATTAGAA	1920	Db	2941	CTTCTTCCGATACAGAAAAAGAGACAGATCACCATCTGCTATATTTTTCAGCAGAGCTG	3000
QY	185	-----	185	QY	186	-----	201
Db	1921	GCITCTCAGTTAATTATGAAGCATAAACATGAGCCTGAAAAACCCCCACCATATGAA	1980	Db	3001	AGTAAACCTTCAGTTCTTGACCTCTCTGTACTGAGAGACATTAAGAAGACTGAGTGGTG	3060
QY	185	-----	185	QY	202	-----	221
Db	1981	GAGGCCATGAGTGATCACTAAAAAAGTATCAGGAATAAGGAAGAAATTAAGAGCCT	2040	Db	3061	TTTGGTCCAGGCTATTTCTGCTGCTTTTATTGACAGATATTCAGCATTGTGACGTAACA	3120
QY	185	-----	185	QY	222	-----	241
Db	2041	GAAAAATTAATGAGCTCTTCAAGAAAACAGAAAGCTCCTTATATATCTATTGTCATGTGAT	2100	Db	3121	GCCTACATTCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTG	3180
Db				QY	242	-----	261



Db	541	TCCTCGGCTCAGTGGATGAGACCCCTTTTGGCTCTTCTCCTGCATCTGAGCCTGTGATA	600
Qy	185	-----	185
Db	601	CGCTCCTCTGCAGAAATATGGACTTGAAGGAGCAGCGCTAACACTATTTCCGGCTGGT	660
Qy	185	-----	185
Db	661	CAAGAGGATTTCCCATCTGCTCCTGCTTGAACCTGCTCTTCTCTCTCTGTCTCCT	720
Qy	185	-----	185
Db	721	CTCTCAGCGCTTCTTTCAAAGACATGAATACCTTGGTAATTTGTCAAAGTATTACCC	780
Qy	185	-----	185
Db	781	ACTGAAGGAACACTTCAAGAAATGTTCAGTGAAGCTTCTAAAGAGGTCTCGAGAGGCA	840
Qy	185	-----	185
Db	841	AAAACTCTACTCATAGATAGAGATTAAACAGAGTTTTTCAGAAATAGAAATCTCAGAAATG	900
Qy	185	-----	185
Db	901	GGATCATGGTTCAGTGTCTCTCAAAGACAGAAATCTCCGTAATAGTAGCAAAATCCTAGG	960
Qy	185	-----	185
Db	961	GAAGAAATAATCGTGAAAAATAAGATGAAGAGAGAAGTTAGTTAGTAATAACATCCTT	1020
Qy	185	-----	185
Db	1021	CATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTG	1080
Qy	185	-----	185
Db	1081	TCTTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAAAGCTCCTATG	1140
Qy	185	-----	185
Db	1141	AGGGAGGATATGCAGACTTCAACCATTTTCAGCGCATATGGGAGTGAAGATAGTAAG	1200
Qy	185	-----	185
Db	1201	GAAGATAGTATATGTTGGCTGCTGGAGTAAATTCGAGAGCAACTTGGAAAGTAAAGTG	1260
Qy	185	-----	185
Db	1261	GATAAAAAATGTTTTGCAGATAGCCTTTGAGCAAACTAATCACGAAAAGATAGTGAGAGT	1320
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Db	1321	AGTAATGATGATACTTCTTTCCCGAGTACGCCAGAGGTATAAGGATCGTCCAGGAGCA	1380
Qy	185	-----	185
Db	1381	TATATCACATGTGCTCCTTTAACCCAGCAGCAACTCGAGAGCATTCGCAACAAATTTTT	1440
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Db	1441	CTTTTGTAGGAGATCCTACTTTCAGAAAAATAAGCCGATGAAAAAAAATAGAGAAAAG	1500
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Db	1501	AAGCCCCAATAGTAAACAGAGAAGATACTAGCNCCAAAAACATCAAAACCTTTTCTTGTA	1560
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Db	1691	AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTT	1740
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Db	1741	CAAAACATCAGAAGTTATGCAAGAGTCACCTCTATCTGCAGACACAGCTTTGCCCATCATTT	1800
QY	185	-----	185
Db	1801	GAAGAGTCAGAAGCTACTCTTCACAGTTTTCCTGCACATTTGTTATGGAAGCACCATTG	1860
QY	185	-----	185
Db	1861	AATCTGCAGTTCCTAGTGTCTGCTCCGTGTACAGCCCGAGCTCATCACCATTAGAA	1920
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Db	1921	GCTTCTTCAGTTAATTATGAAAAACATAAAACATGAGCCTGAAAAACCCCCACCATATGAA	1980
QY	185	-----	185
Db	1991	GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAGGAAGAAATTAAGAGCCT	2040
QY	185	-----	185
Db	2041	GAATAATTAAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATCTATTCATGTGATGAT	2100
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Db	2101	TTAATTAAAGAAACAAAGCTTTCTGCTGAACAGCTCCGGATTTCTCTGATTATTCAGAA	2160
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Db	2161	ATGGCAAAAGTTGAACAGCCAGTCCTGATCATTTCTGAGCTAGTTGAAGATTCCTCACCT	2220
QY	185	-----	185
Db	2221	GATTCTGAACCAAGTTGACTTATTTAGTGATGATTCATACCTGACGTTCCACAAAAACAA	2280
QY	185	-----	185
Db	2281	GATGAACCTGTGATGCTGTGTGAAGAAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA	2340
QY	185	-----	185
Db	2341	GAATATGAATAAAGAAAAAATCAGTGTCTTGCCACCTGAGGGAGGAAAGCCATATTTG	2400
QY	185	-----	185
Db	2401	GAATCTTTTAAGCTCAGTTTAGATAAACAAAAAGATACCTCTGTACCTGATGAAGTTTCA	2460
QY	185	-----	185
Db	2461	ACATTGACAAAAAGGAGAAAAATTCCTTTCAGATGGAGGAGCTCAGTACTGCAGTTTAT	2520
QY	185	-----	185
Db	2521	TCAATGATGACTTATTTATTTCTAAGGAAGCAGACAGATAAGAGAAATCGAAACGTTTTCA	2580
QY	185	-----	185
Db	2581	GATTCACTCCAAATTGAATATATAGATGAGTTCCCTACATTCGATCAGTTCTTAAACTGAT	2640
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Db	2641	TCATTTTCTAAATTAGCCAGGAATATACTGACCTAGAAGTATCCACAAAAAGTGAAAT	2700
QY	185	-----	185
Db	2701	GCTAATGCCCGGATGGAGCTGGGTCAITGGCTTGCACAGAAATGCCCATGACCTTCT	2760

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QY 185 ----- 185
Db 2761 TTGAAGAACATACAAACCAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTATAA 2820
QY 185 ----- 185
Db 2821 AATGGGTCTGTACATCAAAAGGTGCTCTTATTGGCTCCAGATGCTTTCTGCTTTGGCCACT 2880
QY 185 ----- 185
Db 2881 CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTTGTGAAGAGAGCTGAGAAAAAA 2940
QY 185 ----- 185
Db 2941 CTTCTTCGATACAGAAAAAGAGGAGACAGATCACCATCTGCTATATTTTCAGCAGAGCTG 3000
QY 186 -----ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal 201
Db 3001 AGTAAAACTTCAGTTGTTGACCTCTGTACTGGAGAGACATTAAAGAAAGACTGGAGTGGTG 3060
QY 202 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221
Db 3061 TTTGTGTCAGGCTATTCTGCTGCTTTTCATTGACAGATTTCAGCATTTGTGAGCGTAACA 3120
QY 222 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGlyVal 241
Db 3121 GCCTACATTGCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTG 3180
QY 242 IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 261
Db 3181 ATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAA 3240
QY 262 ValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 281
Db 3241 GTTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAAATCTGCTCTTGCTCATGTGAAC 3300
QY 282 CysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLys 301
Db 3301 TGCACGATAAAGAACTCAGGGCCCTCTTCTTAGTTGATGATTAGTTGATTTCTCTGAAG 3360
QY 302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321
Db 3361 TTTGCAGTCTGATGTGGGTATTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTA 3420
QY 322 LeuIleLeuAlaIleSerLeuPheSerValProValIleTyrCluArgHisGlnAla 341
Db 3421 CTGATTTTGGCTCTCATTTTCATCTCTCAGTGTCTCTGTTTATTATGAACGGCATCAGGCG 3480
QY 342 GlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 361
Db 3481 CAGATAGATCATTAICTAGGACTTGGCAATATAGAATGTTAAAGATGCTATGGCTAAATC 3540
QY 362 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
Db 3541 CAAGCAAAAAATCCCTGGATTGAAGGCCAAAGCTGAA 3576
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Search completed: August 3, 2005, 23:25:47  
Job time : 606 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:13:53 ; Search time 3100 Seconds  
 (without alignments)  
 4579.991 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDDQSLVSSSDSPRPQ.....VKDAMAKIOAKIFGLRRKAE 373

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DSV=xlp

-Q=/cp2 1/USPTO spool\_p/US09544776/runat\_03082005\_181345\_28214/app.query.fasta\_1.519

-DB=EST -QPMI=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US09544776 @CGN 1 1 5180 @runat\_03082005\_181345\_28214 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

4: gb\_est3.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_gss1.\*

9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1532.5	80.2	3533	AK034902	Mus muscu
2	1281	67.1	1037	EX439214	EX439214
3	1206	63.1	911	AL549191	AL549191
4	1138.5	59.6	781	BI079496	BI079496
5	1050	55.0	677	CN791158	CN791158
6	999.5	52.3	1002	EX462171	EX462171
7	998	52.3	924	BU845601	BU845601
8	989.5	51.8	708	BI157842	BI157842
9	981.5	51.4	810	BI080232	BI080232

10	948.5	49.7	592	7	CN482802
11	948.5	49.7	990	4	BI691132
12	945	49.5	650	6	CB215381
13	940	49.2	585	2	CO259245
14	937.5	49.1	815	2	BF099705
15	936.5	49.0	958	4	BM801698
16	932.5	48.8	679	4	BI149602
17	928	48.6	598	7	CF118424
18	925	48.4	712	7	CK971318
19	923	48.3	667	7	CN429712
20	917	48.0	600	9	AY404970
21	917	48.0	672	7	CK977984
22	917	48.0	682	6	CB162885
23	917	48.0	743	6	CD102817
24	917	48.0	758	4	BG697436
25	917	48.0	788	1	AL533461
26	917	48.0	843	4	BG570231
27	917	48.0	849	7	CR765672
28	917	48.0	875	1	AL573494
29	917	48.0	1540	3	CR611869
30	917	48.0	1785	3	AF077050
31	914	47.9	730	1	AU297347
32	911	47.7	634	6	CB067821
33	911	47.7	670	7	CV030029
34	911	47.7	960	7	CN646472
35	911	47.7	983	7	CN803408
36	911	47.7	1031	7	CN647521
37	905	47.4	805	7	CO735185
38	904	47.3	757	4	BG715173
39	903	47.3	1042	7	CN805577
40	902	47.2	871	6	CD110203
41	902	47.2	882	5	BX426505
42	901	47.2	600	9	AY404972
43	898	47.0	1013	7	CO048918
44	898	47.0	1018	7	CN801888
45	895	46.9	779	7	CO401465

#### ALIGNMENTS

#### RESULT 1

AK034902

LOCUS

DEFINITION

AK034902 3533 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 12 days embryo embryonic body between diaphragm region  
 and neck cdna, RIKEN full-length enriched library, clone:9430059L06  
 product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN)  
 (POCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus  
 norvegicus], full insert sequence.

ACCESSION

VERSION AK034902.1 GI:26084268

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 20499374

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ighii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,



QY 340 GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAenLysAenVallysAspAlaMetala 359  
|  
|  
Db 1202 CAGCGCAGATAGATCATATTCTTAGGACTTGCAACAAGACGGTTAAGGATGCCATGCC 1361  
|  
|  
QY 360 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373  
|  
|  
Db 1262 AAAATCCAGCAAAAATCCCTGGATTGAAGCGCAAGACAGAA 1303  
|  
|

RESULT 2  
BX439214 1097 bp mRNA linear EST 04-MAY-2004  
LOCUS BX439214 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YG04  
DEFINITION 5'-PRIME, mRNA sequence.  
ACCESSION BX439214  
VERSION BX439214.2 GI:47020895  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1097)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi:30787776.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

This sequence belongs to sequence cluster 1423.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0DE008BD02QP1&c=1423.r>.  
Location/Qualifiers  
1..1097  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE008YG04"  
/tissue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"  
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN  
Alignment Scores:  
Pred. No.: 3,86e-73 Length: 1097  
Score: 1281.00 Matches: 256  
Percent Similarity: 87.97% Conservative: 0  
Best Local Similarity: 87.97% Mismatches: 35  
Query Match: 67.07% Indels: 0  
DB: 5 Gaps: 0

US-09-544-776-2 (1-373) x BX439214 (1-1097)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20  
|  
|  
Db 212 ATGGAGACCTGACCACGTCTCTGTGTCCTCGACACGCCACCACCCGCGGCAG 271  
|  
|

QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
|  
|  
Db 272 CCCGCGTTCAAGTACAGTTCTGTCGAGGAGCCCCGAGGACGAGGAGGAGGAG 331  
|  
|

QY 41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60  
|  
|  
Db 332 GAAGAGGAGCACGAGCACCAAGACCTCGAGAGCTGGAGTGCTGGAGAGAACCCGCC 391  
|  
|

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1423.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?e=CS0DI051CA06QP1&c=1423.r.

## FEATURES

## source

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1. 911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI051YB11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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## ORIGIN

Alignment Scores:  
Pred. No.: 2,2e-68 Length: 911  
Score: 1206.00 Matches: 243  
Percent Similarity: 93.8% Conservative: 1  
Best Local Similarity: 93.46% Mismatches: 15  
Query Match: 63.14% Indels: 1  
DB: 1 Gaps: 0

US-09-544-776-2 (1-373) x AL549191 (1-911)

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QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20
DB 134 ATGGAGACTGGACCAAGTCCTCTGTGTCCTCGTCTGGACAGCCACCCCGCGCGAG 193
QY 21 ProAlaPheLysTyGlnPheValArgGluProGluAspGluGluGluGluGlu 40
DB 194 CCGCGGCTTCAAGTACCAGTTCGTGGAGGAGCCGAGGACGAGGAGGAGGAGGAG 253
QY 41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
DB 254 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 313
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
DB 314 GCGGGGCTCTCGCGGCCCCAGTGGCCACCGCCCTCGCGCGCGCGCCCTGTATGGAC 373
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProVal 100
DB 374 TTCCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCGCCGTC 433
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
DB 434 GCGCGGAGCGGAGCGCGCTTGGGAGCCGAGCCCGGTGCTGTMGACCGTGGCCGCCA 493
QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
DB 494 TCCCGCTGTCTGTGCGCAGTCTCGCCCTCCAAAGTCCCTCGAGGACGACGAGCTTCG 553
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
DB 554 GNCGGGCHTMMHCCTAADYACMMGGCCAGCGTGAACCCCGCCGAGCGCGCGTGTG 613
QY 161 ProProAlaProAlaProAlaProAlaProSerThrProAlaAlaProLysArgGln 180
DB 614 CCGSAGCCCGGCTCSCCGCGGCCCCCTCAACCCCGCGCGCGCGCGCGCGCGCGCG 673
QY 180 ySerSerGlySerValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyVa 200
DB 674 CTCCTCGGCTCAGTGTGTTGTGACCTCTGCTGCTGAGAGAGACATTAAGAGACTGGAGT 733
QY 200 lValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVa 220
DB 734 GGTGTTGTGTGCAGCCTATTCTGCTGCTTTTACATTGACAGTATTGACCATTTGTGAGCGT 793

```

```

QY 220 lThrAlaTyrlleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrlLysG1 240
DB 794 AACAGCCATACATTGCTTGGCCCTCTCTGTGACCATCGCTTCTAGATATACAAGG 853
QY 240 yValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGlu 259
DB 854 TGTGATCCAGCTATCCAGAAATCAGATGAAGCCCAATTCAGGGCATATCTGGAA 911

RESULT 4
BI079496
LOCUS
DEFINITION
602876306F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008248 5',
mRNA sequence.
BI079496
ACCESSION
BI079496.1 GI:14497826
VERSION
EST.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 781)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11052 row: k column: 01
High quality sequence stop: 773.
FEATURES
Location/Qualifiers
1..781
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5008248"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
ORIGIN

Alignment Scores:
Pred. No.: 4,27e-64 Length: 781
Score: 1138.50 Matches: 239
Percent Similarity: 89.36% Conservative: 5
Best Local Similarity: 87.5% Mismatches: 14
Query Match: 59.61% Indels: 15
DB: 4 Gaps: 4

US-09-544-776-2 (1-373) x BI079496 (1-781)
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
DB 3 GCGCCCTGAGAGGACGCCGTCTCTGGAGACGACGCCCGCGCGCTCC-----GCGCCA 53
QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
DB 54 TCCCTCGCGCGCGCTGCGCGAGTCTGCTCCAGCTCCCGAGGACGACGAGCCTCCA 113
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
DB 114 GCGCGG-----CCTCGCGCGCGCGAGCGCGCGCGCTAGCGGAG----- 155

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Db      549 AATGGTCTGACACTACTAATTTTGGCTCTGATTTTCACCTCTTCAGTCTTCTCTGTTATTAT 608
QY      337 GluA9HisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 356
Db      609 GAACGGCATCAGCGCAATAGATCATTTATCTGGGACTTGGCAATTAAGAATGTTAAAGAT 668
QY      357 AlaMetAla 359
Db      669 GCTATGGCT 677

RESULT 6
LOCUS   BX462171
DEFINITION BX462171 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
Clone CS0DG002YP16 5-PRIME, mRNA sequence.
ACCESSION BX462171
VERSION   BX462171.2 GI:47071945
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31035379.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DGO02DH08QP1&c=1423.r.
FEATURES
source
Location/Qualifiers
1..1002
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/clone="CS0DG002YP16"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5,75e-55 Length: 1002
Score: 999.50 Matches: 223
Percent Similarity: 76.00% Conservative: 5
Best Local Similarity: 74.33% Mismatches: 46
Query Match: 52.33% Indels: 28
DB: 5 Gaps: 4

US-09-544-776-2 (1-373) x BX462171 (1-1002)

QY      1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
Db      145 ATGGAAGACCTCGACCACTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 204
QY      21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGl 40
Db      205 CCCCGGTTCAAGTACCACTGCTGTGAGGGAGCCGCGAGGACGAGGAGGAAGAGGAGGA 264

```

```

QY      40 uGluGluGluAspGluAspGluAspGluGluGluValLeuGluValLeuGluValLeuGluValLeu 60
Db      265 GGAAGAGGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGAC 324
QY      60 aAlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAs 80
Db      325 CGCGCGGCTGTCTCGCGGCCCGCCAGTCCACACCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 384
QY      80 pPheGlyAsnAspPheValProAlaProArgGlyPheLeuProAlaProAlaProAlaProVal 100
Db      385 CTTTCGAAATGACTTCGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 444
QY      100 lAlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPr 120
Db      445 CGCCCCGAGAGCGGACGCGCTCTTGGACCCGAGCCCGGTGCTGCTGACCGTCCCGCGCGCGCG 504
QY      120 oSerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPr 140
Db      505 ATCCCGCGTGTCTGCTGCGCGAGTCTCGCCCTCCAAAGCTCCCTGAGGACGAGGAGGCTCC 564
QY      140 oAla-----ArgProProProProProProProProProProProProProProProPro 151
Db      565 GCGCGGTTTTCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTC 601
QY      151 lSerProGlnAlaGluProValTyrThrProAlaProAlaProAlaProAlaProProSe 171
Db      602 -----AGCAAAACCGTGTGDC-CCGCCARC-CCCGCCCCCGGGSSSSSSRS 649
QY      171 rThrProAlaProLysArgArgGlySerGlySerValValValValValValValValValVal 191
Db      650 CCGSGGGGCGCMAG-----CSMGGGGCGCCCGGSYCA---GTGGTGKTGACCCCGTA 697
QY      191 rTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSe 211
Db      698 CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCACGCTATTCCTCTGCTCTTC 757
QY      211 rLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerVa 231
Db      758 ATTGACAGTATTCAGCATTTGTGAGGCTAACAGCTACATTGCTTGGCCCTCTCTCTGT 817
QY      231 lThrIleSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGl 251
Db      818 GACCATCAGCTTAGCATATACAGGGTGTGATCAAGCTATCCAGAAATCAGATGAARG 877
QY      251 yHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnly 271
Db      878 SCMCCCATTCAGGGGATATTTGGGAWTGAATTTKSTATATTTKRRGGGKTGGTCARAA 937
QY      271 stYrSer-AsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 289
Db      938 AWAATAAATTTTKSTCTTGGKCATDTTAAWTHSACVAAWAAARAAWCAAGCG 993

RESULT 7
BU845601
LOCUS   BU845601
DEFINITION AGENCOURT 10414454 NIH MGC 109 Homo sapiens cDNA clone
IMAGE:6575264 5', mRNA sequence.
ACCESSION BU845601
VERSION   BU845601.1 GI:24030042
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
NIH-MGC http://mgi.cni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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QY 166 ProAlaAProProSerThrProAlaAProLysArgArgGlySerSerGlySerVal 185
Db 2 CCCGCCGCCCCCTTCACAGCGCGCGCCGCAAGCGAGCGGC---TCGGGCTCAGTG 58
QY 186 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 205
Db 59 GTTGTGTGACCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTCGTGCCAGC 118
QY 206 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 225
Db 119 TTATTCTCTGCTGCTCTGCAGCTGTTTCAGCAATGTTCAGTGAACGGCTACATTGCC 178
QY 226 LeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIle 245
Db 179 TTGGCCCTCTCTGTGACTATACGCTTGGATATATAAGGGTGTGATCAAGCTATTC 238
QY 246 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 265
Db 239 CAGAATCAGATGAGGCCACCCATTCAGGGCATATTTGGAATCTGGAAGTTCGCATATCA 298
QY 266 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnCysThrIleLys 285
Db 299 GAGGAATTGGTTTCAGAAATATAGTAATTCCTGCTCTTGGTTCATGTGAACAGCAATAAAA 358
QY 286 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 305
Db 359 GAATTGAGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTCAAGTTTCAGTTGCTG 418
QY 306 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 325
Db 419 ATGTGGGTATTACTTACGTTGGTGGTCTTGTTCATTTGTTGACACTACTGATTTTAGCT 478
QY 326 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 345
Db 479 CTGATCTCACTCTTCAGTATTCTCTGTATATATATGAACGGCATCAGCGCGAGATGATCAT 538
QY 346 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 365
Db 539 TATCTAGGACTTGCACAAAGAGCGTTAAGGATGCCATGCCCAAAATCCAGCAAAATC 598
QY 366 ProGlyLeuLysArgLysAlaGlu 373
Db 599 CCTGGATTGAAGCGCAAGACAGAA 622

RESULT 9
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LOCUS
DEFINITION BI080232 810 bp mRNA linear EST 20-JUN-2001
602876650F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008092 5',
mRNA sequence.
ACCESSION BI080232
VERSION BI080232.1 GI:14498562
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: L14W11052 row: d column: 13
High quality sequence stop: 802.
Location/Qualifiers
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/clone="IMAGE:5008092"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 6,49e-54 Length: 810
Score: 981.50 Matches: 227
Percent Similarity: 86.03% Conservative: 7
Best Local Similarity: 93.46% Mismatches: 17
Query Match: 51.39% Indels: 22
DB: 4 Gaps: 4

US-09-544-776-2 (1-373) x BI080232 (1-810)
QY 107 SerTrpAspProSerProValSerSerThrValProAlaProSerPheLeuSerAlaAla 126
Db 2 TCCTGGGAACGAGCCCGCGCGGTCC-----GCGCCATCCCTCGCGCCCGCTGCC 52
QY 127 AlaValSerProSerLysLeuProGluAspGluProProAlaArgProProPro 146
Db 53 GCAGTCTCTCCCTCAAGCTCCCGGAGGACGACGAGCTCCAGCGCGG-----CCTCG 106
QY 147 ProProAlaSerValSerProGlnAlaGluProValThrProProAlaProAlaPro 166
Db 107 GCGCCAGCGCGCGCGAGCCCTCCTAGCGAG-----CCC 139
QY 167 AlaAlaProProSerThrProAlaAlaProLysArgArgGlySerSerGlySerVal 186
Db 140 GCGCGCGCCCTTCACCGCGCGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 196
QY 187 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 206
Db 197 GTTGACCTCTCTGACTCGGAGAGACATTAAGAAGACTGGAGTGGTGTTCGTGCCAGCTTA 256
QY 207 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 226
Db 257 TTCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAAGCGGCTTACATTGCCCTTG 316
QY 227 AlaLeuLeuSerValThrIleSerProArgIleTyrLys-GlyValIleGlnAlaIle 246
Db 317 GCGCTGCTCTCTGACTATCAGCTTTAGGATATATAACGGGTGTGATCCAGCTATCCA 376
QY 246 nLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 266
Db 377 GAAATCAGATGAAGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTCGCATATCAGA 436
QY 266 uGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys-G 286
Db 437 CGAAATGGTTTCAGAAATATAGTAATTCCTGCTCTTCGTTCATGTGAACAGCACACAAACAG 496
QY 286 luLeuArgArgLeuPheLeuValAsp-AspLeuValAspSerLeuLysPheAlaVal-Le 305
Db 497 ACTTGAGCGGCTCTCTCTTAGCTGACTGATTTAGTTGATTCCTGAGTTTGCAGTGTCG 556
QY 305 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 325
Db 557 ACTGTGGGTATTTACTTACGTTGGTGC-CTGTTCAATGGTTTGACACTACTGATTTCCAG 615
QY 325 aleuIleSerLeuPheSerValProVal-IleTyrGluArg-HisGlnAlaGlnIleAsp 344
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/lab_host="DH108"
/clone_lib="NCI_CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Alignment Scores:
Pred. No.: 1.13e-51 Length: 990
Score: 948.50 Matches: 200
Percent Similarity: 97.13% Conservative: 3
Best Local Similarity: 95.69% Mismatches: 4
Query Match: 49.66% Indels: 3
DB: 4 Gaps: 1

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DB 7 CCGCGCGCGCCCTTCACGCGCGCGCGCGCGCGAG-GGC---TCGGGCTCAGTG 62
QY 186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 205
DB 63 GTTGTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGTGTTGGTCCAGC 122
QY 206 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrIleAla 225
DB 123 TTATTCTCTGCTGTCTGTGACAGTGTTCAGCATTTGTGAGTAAACGCCCTACATTGCC 182
QY 226 LeuAlaLeuLeuSerValThrIleSerProArgIleTyrLys-GlyValIleGlnAla 245
DB 183 TTGGCCCTCTCTGTGACTATCAGCTTAGATATATAACGGGTGTGATCCAGCTAT 242
QY 245 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 265
DB 243 CCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCTGAAGTTGCCATATC 302
QY 265 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
DB 303 AGAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTTGTGTCATGTGAACAGACACATAAA 362
QY 285 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 305
DB 363 AGAATTGAGCGGTCTCTCTTGTAGTGATTTAGTTGATTCCTGAAAGTTTGCAGTGT 422
QY 305 uMetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAl 325
DB 423 GATGTGGGTATTACTTACGTGGTGGCTTGTTCATATGTTTGACACTACTGATTTTAGC 482
QY 325 aLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 345
DB 483 TCTGATCTCACTCTTCAGTATCTCTGTATATATGAACGGCATTCAGGCGCATAGATCA 542
QY 345 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 365
DB 543 TTATCTAGGACTTGCAACAGAGCGTTAAGATGCAATGGCCAAATCCAAAGCAAAAT 602
QY 365 eProGlyLeuLysArgLysAlaGlu 373
DB 603 CCTGGATTGAAGCGCAAGAGCAA 627

RESULT 12
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DEFINITION
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5', mRNA sequence.
ACCESSION
CB215381
VERSION
CB215381.1 GI:28263573
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[infoimage.llnl.gov](mailto:infoimage.llnl.gov)  
Plate: L14M13163 row: G column: 23  
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/clone="IMAGE:5937070"  
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/note="Organ: uterus; Vector: pCMV-SPORT6.1.cdb (ResGen,  
Invitrogen Corporation); Site 1: NotI; Site 2: EcoRV;  
Cloned unidirectionally from microquantity amounts of mRNA  
from normal endometrial tissue (late proliferative phase,  
cycle day 13). Average insert size 1.9 kb. Library  
constructed by ResGen (Invitrogen Corporation)."  
Alignment Scores:  
Pred. No.: 1.14e-51 Length: 650  
Score: 945.00 Matches: 193  
Percent Similarity: 99.48% Conservative: 0  
Best Local Similarity: 99.48% Mismatches: 1  
Query Match: 49.48% Indels: 0  
DB: 6 Gaps: 0  
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QY 200 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 219  
DB 61 GTGGTGTGTGGGCGCAGCGCTATCTCTGCTGCTTTTATTGACAGATATTCAGCAATTGGAGC 120  
QY 220 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLys 239  
DB 121 GTAACAGCTCATTTGCCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAG 180  
QY 240 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 259  
DB 181 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAA 240  
QY 260 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis 279  
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QY 280 ValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSer 299  
DB 301 GTGAACCTGCAGATTAAGGAACCTCAGGCGCTCTTCTTAGTTGATGATTTAGTATTCT 360  
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Db      361 CTGAAGTTTCAGTGTGATGTGGTATTTACCTATCTGTGGTGCCTTTTAATGCTCTG 420
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Db      421 ACCTACTGATTTGGCTCTCATTTCTACTTCTGATGTTCTGTATTTAAGACGGCAT 480
Qy      340 GlnAlaGlnIleAepHisTyrLeuGlyLeuAlaAenLysAenVallysAepAlaMetAla 359
Db      481 CAGGACAGATAGATCATTTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCT 540
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Db      541 AAAATCCAGCAAAATCCCTGGATTGAAGCGAAAGCTGAA 582

RESULT 13
LOCUS   CO259245
DEFINITION 585 bp mRNA linear EST 23-JUN-2004
sequence. 4130444 BARC 8BOV Bos taurus cDNA clone 8BOV_51K20 5', mRNA
ACCESSION CO259245
VERSION    CO259245.1 GI:49144047
KEYWORDS  EST.
SOURCE    Bos taurus (cow)
ORGANISM  Bos taurus
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          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 585)
AUTHORS  Baumann,R.G.; Baldwin,R.L.; Sonstegard,T.S.; Van Tassell,C.P. and
          Matukumalli,L.K.
TITLE    Construction and Analysis of a cDNA Library Generated From
          Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL  Unpublished (2004)
COMMENT  Contact: Richard G. Baumann
          Bovine Functional Genomics Lab
          ANRI
          BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
          Tel: 3015048604
          Fax: 3015048744
          Email: rbaumann@anri.barc.ueda.gov
          Single pass sequencing. Bases called and trimmed with phred
          0.000925 using options -trim_alt -trim_fasta. Vector identified
          by cross match using options -minmatch 12 -minscore 12
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            /clone_lib="BARC 8BOV"
            /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site: 1:
            Noti; Site 2: EcoRI; Normalized cow cDNA intestinal
            library in pCMVSPORT6.1, constructed from equimolar mRNA
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            neonatal intestinal 4/5 Lactating, Proximal Duodenum,
            Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
            Duodenum, Jejunum, Distal Ileum"
ORIGIN
Alignment Scores:
Pred. No.: 2.12e-51 Length: 585
Score: 940.00 Matches: 192
Percent Similarity: 98.97% Conservative: 0
Best Local Similarity: 98.97% Mismatches: 2
Query Match: 49.21% Indels: 0

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DB:      7      Gaps: 0
US-09-544-776-2 (1-373) x CO259245 (1-585)
Qy      176 ProLysArgArgGlySerValValValAspLeuLeuTyrTrpArgAspIle 195
Db      2   CCACAAACGCGGGGCTCTCGGGCTCAGTGGTTGTTGACCTCTCTACTGGAGACATT 61
Qy      196 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 215
Db      62  AAGAAGACTGGAGTGGTGGTCCGGTGCAGCTGTTCTCTGCTGCTCGCTGACAGTATTC 121
Qy      216 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPro 235
Db      122 AGCATTTGTGAGTGAACGGCTACATTGCTTGGCCCTGCTCTCTGTGACTATCAGCTTT 181
Qy      236 ArgIleTyrIysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 255
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Qy      256 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 275
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Qy      276 AlaLeuGlyHisValAenCysThrIleLysGluLeuArgArgLeuPheLeuValAspAep 295
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Qy      296 LeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeu 315
Db      362 TTAGTTTGAATTTCTTGAAGTTTGAGTGTGATGTTGGGTATTTACCTATGTTGGTCTTG 421
Qy      316 PheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIle 335
Db      422 TTCATGTTGCTGCACACTACTAATTTTGGCTCTGATTTCACTCTCTCAGTGTCTCTGTATT 481
Qy      336 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAenLysAenValLys 355
Db      482 TATGAACGGCATCAGCGCAAAATAGATCATTTATCTGGGACTTCGCAATTAAGATGTAAA 541
Qy      356 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 369
Db      542 GATGCTATGGCTAAATAATCCAGCAAAATCCCTGGATTGAAG 583

RESULT 14
LOCUS   BF099705
DEFINITION 815 bp mRNA linear EST 19-OCT-2000
mRNA sequence.
ACCESSION BF099705
VERSION    BF099705.1 GI:10882231
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 815)
AUTHORS  NIH-MGC http://mgi.nci.nih.gov/
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM9172 row: 0 column: 10
          High quality sequence stop: 712.
          Location/Qualifiers
            1..815
FEATURES
          source

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QY 245 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 264
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QY 265 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 284
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Db 303 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAAATCTGCTCTTGGTCATGTGAACAGTCACGATA 362
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QY 285 LysGluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 304
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Db 363 AAGAACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAAGTG 422
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QY 305 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 324
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Db 423 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTGACACTACTGATTTTG 482
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QY 325 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 344
    |||||
Db 483 GCTCTCATTTTCACTCTTCACTGTTCCCTGTTATTTATGAAACGGCATCAGGCACAGATAGAT 542
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QY 345 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 364
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Db 543 CATTATCTACGACTTGCAAAATAGAAATGCTAAAGATGCTATGGCTAAATCCAAGCAAAA 602
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QY 365 IleProGlyLeuLysArgLysAlaGlu 373
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Search completed: August 4, 2005, 00:29:15  
Job time : 3113 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:13:52 ; Search time 207 Seconds

(without alignments)  
2948.460 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDDQSPVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRAE 373

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPRO\_spool\_p/US09544776/runat\_03082005\_181346\_28231/app\_query.fasta\_1.519

-DB=Issued Patents NA -Qfmt=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=us09544776 @CGN 1.1.105 @runat\_03082005\_181346\_28231 -NCPU=6 -ICPU=3

-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*

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5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	917	48.0	1669	4	Sequence 2, Appli
4	904	47.3	2610	4	Sequence 3253, Ap
5	747.5	39.1	2069	4	Sequence 382, App
6	747.5	39.1	3202	4	Sequence 389, App
7	672.5	35.2	1766	3	Sequence 1127, Ap
8	659.5	34.5	2664	3	Sequence 254, App
9	613.5	32.1	2262	4	Sequence 255, App
10	550	28.8	1095	2	Sequence 2988, Ap
11	547	28.6	3517	4	Sequence 4, Appli
12	541.5	28.4	794	3	Sequence 111, App
					Sequence 102, App

13	527.5	27.6	2181	4	US-09-949-016-1419	Sequence 1419, Ap
14	513	26.9	2014	4	US-09-270-767-13561	Sequence 13561, A
15	347	18.2	441	4	US-09-513-999C-2227	Sequence 2227, Ap
16	344.5	18.0	454	4	US-09-621-976-740	Sequence 740, App
17	344.5	18.0	463	4	US-09-621-976-741	Sequence 741, App
c 18	332	17.4	601	4	US-09-949-016-117588	Sequence 117588,
c 19	332	17.4	601	4	US-09-949-016-117589	Sequence 117589,
c 20	332	17.4	42075	4	US-09-949-016-14995	Sequence 14995, A
21	301	15.8	443	4	US-09-513-999C-3784	Sequence 3784, Ap
22	275	14.4	261	2	US-08-700-607-9	Sequence 9, Appli
23	269.5	14.1	135667	4	US-09-949-016-15051	Sequence 15051, A
24	269.5	14.1	152486	4	US-09-949-016-12869	Sequence 12869, A
c 25	266	13.9	601	4	US-09-949-016-40169	Sequence 40169, A
c 26	266	13.9	601	4	US-09-949-016-119335	Sequence 119335,
c 27	257	13.5	13906	4	US-09-949-016-14730	Sequence 14730, A
28	256	13.4	200	4	US-09-513-999C-11198	Sequence 11198, A
29	246	12.9	15661	4	US-09-949-016-13161	Sequence 13161, A
c 30	217	11.4	2580	3	US-09-050-863-2	Sequence 2, Appli
c 31	217	11.4	2580	3	US-09-359-081-2	Sequence 2, Appli
c 32	217	11.4	8705	4	US-09-647-344A-14	Sequence 14, Appli
c 33	217	11.4	9600	3	US-08-910-647-1	Sequence 1, Appli
c 34	217	11.4	9600	3	US-09-620-925-1	Sequence 1, Appli
c 35	217	11.4	10596	1	US-07-884-811-15	Sequence 15, Appl
c 36	217	11.4	10596	1	US-07-885-971-15	Sequence 15, Appl
c 37	217	11.4	10596	1	US-08-087-783A-15	Sequence 15, Appl
c 38	217	11.4	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 39	217	11.4	10596	2	US-08-194-087-15	Sequence 15, Appl
c 40	217	11.4	10596	5	PCT-US93-04648-15	Sequence 15, Appl
41	217	11.4	16080	4	US-09-724-566A-48	Sequence 48, Appl
42	217	11.4	16080	4	US-09-471-669A-48	Sequence 48, Appl
43	212	11.1	5452	2	US-09-130-114-1	Sequence 2, Appli
c 44	210	11.0	1926	3	US-09-249-585A-2	Sequence 2, Appli
c 45	210	11.0	1926	4	US-09-410-399-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

; Patent No. 6426186

; GENERAL INFORMATION:

; APPLICANT: Jones, Karen A.

; APPLICANT: Volkmut, Wayne

; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES

; FILE REFERENCE: PB-0014 US

; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PERL Program

; SEQ ID NO 106

; LENGTH: 4822

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1

; NAME/KEY: unsure

; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,

; OTHER INFORMATION: a, t, c, g, or other

US-09-484-970B-106

Alignment Scores:

Pred. No.: 2.69e-89 Length: 4822

Score: 1431.00 Matches: 365

Percent Similarity: 30.68% Conservative: 1

Best Local Similarity: 30.60% Mismatches: 7

Query Match: 74.92% Indels: 820

DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x US-09-484-970B-106 (1-4822)

QY	1	MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProArgProGln	20
Db	253	ATGGAAAGACTGGACGAGTCTCTCTGGTCTCGTCTCGACAGCCACCCCGCGCGAG	312
QY	21	ProAlaPheLysTyrglnPheValArgGluProGluAspGluGluGluGluGluGlu	40
Db	313	CCCGGCTTCAAGTACCAGTTCTGTGGGAGCCGAGGACGAGGAGGAAGAGGANGAT	372
QY	41	GluGluGluAspGluAspGluAspLeuGluLeuGluValLeuGluArgLysProAla	60
Db	373	GAAGAGGAGGACGAGGACCAAGACCTGGAGGAGCTGGAGGTCTGGAGAGGAGCCCGCC	432
QY	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyValaProLeuMetAsp	80
Db	433	GGCGGGCTGTCGGGGCCCCAGTGCACCGCCCTGCGCCGCGCGGCNNNTAATGGAC	492
QY	81	PheGlyAsnAspPheValProProAlaProAlaProArgGlyPheLeuProAlaAlaProVal	100
Db	493	TTTCGGAATGACTTCTGTGCGCGCGCGCCCGGGGACCCCTCGCGCGCTCCCCCGGTC	552
QY	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
Db	553	GCCCGGAGCGGACGCCGCTTTGGGACCGCGCGCGGTGTCGTCAACCGTGCCTCGGCCA	612
QY	121	SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro	140
Db	613	TCCCGCTGTCTGTGCGCGCAGTCTCGCCCTCAAGTCTCCCTGAGGACGACGAGCTCCG	672
QY	141	AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
Db	673	GCCCGGCTCCCTCTCCCGCGCACGCTGAGCCCGCCAGGACGAGCCCTGTGGANC	732
QY	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgGly	180
Db	733	CGGCCAGCCCCGGCTNCGCGCGCGCCCCCTCCACCCGCGCGCCCAAGCGCAGGGGC	792
QY	181	SerSerGlySerVal	185
Db	793	TCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTCTCTCTGTCATCTGAGCCTGTGATA	852
QY	185	-----	185
Db	853	CGCTCCTCTGCAGAAAAATAGCATTTGAAGGAGCAGCAGGTAAACACTATTTTCGGCTGT	912
QY	185	-----	185
Db	913	CAAGAGATTTCCTCATCTGTCTGTGTTGAACTGCTGTCTCTCTCTCTCTCTCTCTCT	972
QY	185	-----	185
Db	973	CTCTCAGCGCTTCTTTCAAGAACATGAATACCTTGGTAAATTTGTCAACAGTATTACCC	1032
QY	185	-----	185
Db	1033	ACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGTCTCAGAGAAGCA	1092
QY	185	-----	185
Db	1093	AAAACTCTACTCATAGATAGATTTAACAGAGTTTTCAGATTAGATTAGATTAGATTAG	1152
QY	185	-----	185
Db	1153	GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAACTGCGCGTAATAGTAGCAAACTCTAGG	1212
QY	185	-----	185
Db	1213	GAAGAAATAATCGTGAAAAATAAAGATGAAGAGAGAGTGTAGTAGTAATACATCTTT	1272
QY	185	-----	185
Db	1273	CATAATCAACAGAGTTTACCTACAGCTCTTACTAAATTTGGTTAAAGAGGATGAAGTTTG	1332
QY	185	-----	185
Db	1333	TCCTCAGAAAAAGCAAAAGACAGTTTTAAATGAAAAGAGATTGCAGTGAAGCTCCTATG	1392
QY	185	-----	185
Db	1393	AGGGAGGAATATGCAGACTTCAAAACATTTGAGCGAGTATGGGAAGTGAAGATAGTAAG	1452
QY	185	-----	185
Db	1453	GAAGATAGTATATGTTGGCTGCTGGAGTAAATCGAGAGCAACTTGGAAAAGTAAAGTG	1512
QY	185	-----	185
Db	1513	GATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTAGACT	1572
QY	185	-----	185
Db	1573	AGTAATGATGATACCTTCTTTCCAGTAGCCGAGGAGGTATAAGGATCGTTTCAGAGCA	1632
QY	185	-----	185
Db	1633	TATATCATGTGTCTCCCTTTAAACCAGAGCAACTGAGAGCATTTGCAACAAACATTTT	1692
QY	185	-----	185
Db	1693	CTTTTGTAGGAGATCTTACTTCAGAAAATAAGACCGATGAAAAAATAAGAAAAA	1752
QY	185	-----	185
Db	1753	GAAGCCCCAAATAGTAAACAGAGAAGATACTAGCACCAAAACATCAAAACCTTTTACTTG	1812
QY	185	-----	185
Db	1813	TAGCAGCAGAGTTCTGAGACAGATTATGTCAACACAGATTAATTAACAAAGGTGACTG	1872
QY	185	-----	185
Db	1873	AGGAAGTCGTGCAAAACATGCCGTGAAGCCTGACTCCAGATTTAGTACAGGAAGCATGTG	1932
QY	185	-----	185
Db	1933	AAAGTGAATTGAATGAAGTTACTGTGTACAAAGATTGCTTATGAAAACAAAAATGGACTTG	1992
QY	185	-----	185
Db	1993	TTCAAAACATCAGAAGTTATGCAAGAGTCACTCTATCTCTGCAGCAGCTTTGCCCATCAT	2052
QY	185	-----	185
Db	2053	TTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTCCTGACATTGTATGGAAGCACCAT	2112
QY	185	-----	185
Db	2113	TGAATTCGCAAGTCTCTAGTGTGTGTTCGTGTATCAGCCAGCTCATCCCATATG	2172
QY	185	-----	185
Db	2173	AAGCTTCTTCAGTTAAATTATGAAAGCATAAACATGAGCCTGAAAACCCCCCACCATATG	2232
QY	185	-----	185
Db	2233	AAGAGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAAGAAATTAAGAGC	2292
QY	185	-----	185
Db	2293	CTGAAAAATTAATGACGCTCTTCAAGAAACAGAGCTCCTTATATATATCTATTGTCATGTG	2352
QY	185	-----	185
Db	2353	ATTTAAATTAAGAAAAAGCTTTCTGTGTGAACAGCTCCGGATTTCTCTGATTATTTCAG	2412
QY	185	-----	185

Db 2413 AAATGGCAAAAGTTGAACAGCCAGTGCCTGATCAATTCCTGAGCTAGTTGAAGATTCCTCAC 2472  
QY 185 ----- 185  
Db 2473 CTGATTCAGACCAAGTTGACTTATTAGTGATGATTAATCACTGAGCTTCCAAAAAC 2532  
QY 185 ----- 185  
Db 2533 AAGATGAAACTGTGATGCTTTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGA 2592  
QY 185 ----- 185  
Db 2593 TAGAATATGAAATAAGAAAACTCAGTGTCTTTGGCCACTGAGGAGAAAGCCATATT 2652  
QY 185 ----- 185  
Db 2653 TGGAAATCTTTAAGCTCAGTTTAGATAACAAAAAGNATACCTGTGTACCTGATGAAGTTT 2712  
QY 185 ----- 185  
Db 2713 CAACATTGAGCAAAAGAGAAAAATTCCTTTGAGATGGAGGAGCTCAGTACTGCAGTTT 2772  
QY 185 ----- 185  
Db 2773 ATTCAATGATGACTTATTATTCTTAAGGAAGCACAGATAAGAAAACTGAAACGTTTTT 2832  
QY 185 ----- 185  
Db 2833 CAGATTCAATCCAAATTGAAATATTAGATGAGTTCCTCATATGATCAGTTCTTAAACTG 2892  
QY 185 ----- 185  
Db 2893 ATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCAAAAAGTGAAA 2952  
QY 185 ----- 185  
Db 2953 TTGCTAATGCCCGGATGGAGCTGGGTCAATGCTTGCAAGAAATGGCCCCATGACCTTT 3012  
QY 185 ----- 185  
Db 3013 CTTTGAAGAACATACAAACCAAGTTGAAGAGAAATCAGTTTCTCAGATGACTTTTCTA 3072  
QY 185 ----- 185  
Db 3073 AAAATGGGTCTGTACATCAAGGTGCTCTTATTGCTCCAGATGTTTCTGCTTTGGCCA 3132  
QY 185 ----- 185  
Db 3133 CTCAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTCTTGTGAAAGAGCTGAGAAA 3192  
QY 185 ----- 185  
Db 3193 AACTTCCTTCGATACAGAAAAGAGGACAGATCACCATCTGTATATTTTCAGCAGAGC 3252  
QY 186 -----ValValAspLeuLeuTyrTyrArgAspIleLeuVal 200  
Db 3253 TGAGCTAAACCTTCAGTTGTGACCTCTGTACTGAGAGACATTAAGAAGACTGGAGTG 3312  
QY 201 ValPheGlyValSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 220  
Db 3313 GTGTTTGGTGGCAGCCTATTCTCGCTGCTTTCAATGACAGTATTCAGCAATGTGACGTA 3372  
QY 221 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrIleGly 240  
Db 3373 ACAGCTTACATGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAGGGT 3432  
QY 241 ValIleGlnAlaIleGlnIleSerAspGluGlyHisProPheArgAlaTyrIleGluSer 260  
Db 3433 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCT 3492  
QY 261 GluValAlaIleSerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisVal 280  
Db 3493 GAAGTTGCTATATCTCAGGAGTTGGTTTGAAGATACAGTAATTTCTGCTCTTGGTCAITG 3552

QY 281 AsnCysThrIleLeuGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu 300  
Db 3553 AACTGCACGATAAAGAACTCAGGCGCTCTCTCTTAGTTGATGATTTAGTTGTTCTCTG 3612  
QY 301 LysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320  
Db 3613 AAGTTTGCAGTGTGATGTGGGTATTACCTATGTTGGTGCCTGTTTAATGGTCTGACA 3672  
QY 321 LeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340  
Db 3673 CTACTGATTTGGCTCTCAATTCATCTTCAGTGTTCCTGTTATTTATGACGGCATCAG 3732  
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360  
Db 3733 GCACAGATAGATCATTTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAA 3792  
QY 361 IleGlnAlaLeuIleProGlyLeuLysArgLysAlaGlu 373  
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RESULT 2  
US-08-700-607-2  
; Sequence 2, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 799 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
; US-08-700-607-2

Alignment Scores:  
Pred. No.: 8.12e-55 Length: 799  
Score: 917.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 48.01% Indels: 0  
DB: 2 Gaps: 0

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US-09-544-776-2 (1-373) x US-08-700-607-2 (1-799)
QY 186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 205
Db 108 GTTGTGACCTCCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCACG 167
QY 206 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 225
Db 168 CTAATTCCTGCTCTTTCATGACGATTAACAGATTGTGAGGCTAACAGCCTACATTGCC 227
QY 226 LeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIle 245
Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287
QY 246 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 265
Db 288 CAGAAATCAGATGAAGGCCACCANTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347
QY 266 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
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QY 286 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 305
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QY 306 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 325
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QY 326 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 345
Db 528 CTCATTTCACTCTTCAGTGTCTGTTATTGAACGGCATCAGGCACAGATAGATCAT 587
QY 346 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 365
Db 588 TATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAGCAAAAATC 647
QY 366 ProGlyLeuLysArgLysAlaGlu 373
Db 648 CCTGGATTGAAGCGCAAGCTGAA 671

RESULT 3
US-09-949-016-3253
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3253
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253
Alignment Scores:
Pred. No.: 2,148-54 Length: 1669
Score: 917.00 Matches: 187
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
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Query Match: 48.01% Indels: 0
DB: 4 Gaps: 0
US-09-544-776-2 (1-373) x US-09-949-016-3253 (1-1669)
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Db 248 GTTGTGACCTCCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCACG 307
QY 206 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 225
Db 308 CTAATTCCTGCTCTTTCATGACGATTAACAGATTGTGAGGCTAACAGCCTACATTGCC 367
QY 226 LeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIle 245
Db 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427
QY 246 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 265
Db 428 CAGAAATCAGATGAAGGCCACCANTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 487
QY 266 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
Db 488 GAGGAGTTGGTTCAGAAGTACAGTAATCTCTCTTTGGTCATGTGAAGTGCACGATAAG 547
QY 286 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 305
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QY 306 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 325
Db 608 ATGTGGGTATTACCTATGTGTGGTCTGTTTAATGGTCTGACACTACTGATTTGGCT 667
QY 326 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 345
Db 668 CTCATTTCACTCTTCAGTGTCTGTTATTGAACGGCATCAGGCACAGATAGATCAT 727
QY 346 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 365
Db 728 TATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAGCAAAAATC 787
QY 366 ProGlyLeuLysArgLysAlaGlu 373
Db 788 CCTGGATTGAAGCGCAAGCTGAA 811

RESULT 4
US-09-023-655-382
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 382:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2610 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: LUNGNOT14
/ CLONE: 1508778
/ US-09-023-655-382

Alignment Scores:
Pred. No.: 3,04e-53 Length: 2610
Score: 904.00 Matches: 187
Percent Similarity: 98.94% Conservative: 0
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 47.33% Indels: 1
DB: 4 Gaps: 0

US-09-544-776-2 (1-373) x US-09-023-655-382 (1-2610)
QY 186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 205
DB 1311 GTTGTGACCTCTGTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCAGC 1370
QY 206 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 225
DB 1371 CTATTCTCTGCTGCTTCAATTCAGCATATTTCAGCATTTGTGAGCGTAACAGCTACAATTGC 1430
QY 225 aLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaI 245
DB 1431 CTTGGGCCCTCTCTGTGACCATCATAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 1490
QY 245 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 265
DB 1491 CCAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGATCTGAAGTTCGTATATC 1550
QY 265 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLy 285
DB 1551 TGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTTGTGTCATGTGAAGTTCACGATAA 1610
QY 285 sGluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 305
DB 1611 GGAACCTCAGCGGCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAGTTTCAGTGTT 1670
QY 305 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl 325
DB 1671 GATGTGGGTATTTACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1730
QY 325 aLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 345
DB 1731 TCTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAAAGCGCATCAGGCACAGATAGTCA 1790
QY 345 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 365
DB 1791 TTAICTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAAT 1850
QY 365 eProGlyLeuLysArgLysAlaGlu 373
DB 1851 CCCTGGGTTGAAGCGCAAAAGCTGAA 1875

RESULT 5
US-09-949-016-3309

/ Sequence 3309, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 3309
/ LENGTH: 2069
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-3309

Alignment Scores:
Pred. No.: 1.45e-42 Length: 2069
Score: 747.50 Matches: 180
Percent Similarity: 54.12% Conservative: 50
Best Local Similarity: 42.35% Mismatches: 113
Query Match: 39.14% Indels: 83
DB: 4 Gaps: 10

US-09-544-776-2 (1-373) x US-09-949-016-3309 (1-2069)
QY 4 LeuAspGlnSerProLeuValSerSerAspSerProArgProGlnProAlaPhe 23
DB 127 CTGGCCGACAGGCCCGAGGTCGAAGGCCAGGTCGCGGACCGCCCAACC----- 171
QY 24 LysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGlu 43
DB 172 -----ATCCCCAGCCCCCTCGACACAGGCGGAGCGGAGTGGGGGAC 219
QY 44 AspGluAspGluAspLeuGluLeuValLeuGluValLysProAlaAlaGlyLeu 63
DB 220 -----TCAGAGATCGAGCTGTGTCGAGGACCCCATGGCGCGGAG 261
QY 64 SerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsn 83
DB 262 GAGCGCTGCCCC-----TCAGGCTATGTGAGCTTTGGCCAC 297
QY 84 AspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal----- 100
DB 298 GTGGCGCGCCCGCGCCCTCG-----CCCGCTCGCCATCCATCCAGTACAGC 345
QY 101 -----AlaProGluArgGln-ProSerTrpAspProSerProValSerThrVal-- 117
DB 346 ATCCTGAGGAGGAGCGCGGCGGCGGAGCTGTCGAGCAGGCTCATCATCGAGTCGTGCGAC 405
QY 118 -----Pr 118
DB 406 GCCTCTCGGCTCGGAGGAGAGCCCAAGCGGAGCAGACTCACCCCGATGAAGCCC 465
QY 118 oAlaPro-----SerPheLeuSerAl 125
DB 466 AGCGCCCTGGATGCCATCCGGGAGGAGACTGGGTCGCGGCGGAGGCGTGGCCCAAGC 525
QY 125 aAlaAlaValSerProSerLysLeuProGluAspAspGluProProAlaArgProPr 145
DB 526 CGGCGGGGCTGCGGAGCGGCGGTTCTCTCTC-GACTACCCCTCACTGAGGCCAGCC 584
QY 145 oPro-----ProProAlaSerValSerProGlnAlaGluProValTrpThrProPr 162
DB 585 TGGCCCGGAGTGGCCCCCTGGAGACGAGCCCTGGAGCGCTGAGAGCCCATGTTGCCACG 644
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QY 162 oAlaPro---AlaProAlaAlaProSerThrProAlaAlaProLysArgGlySe 181
Db 645 GAAGCTGAGAGACTCGAGTTCACAAAGTCTCGGGCCACAAAGGGCCCTGGGCC 704
QY 181 rSerGly-----SerValValValAspLeu 189
Db 705 TCTAGTCTCGGGCCGCCCCCACTGCTGTTTCTCAATAAGCAAAAGCTATTGACCT 764
QY 189 uLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLe 209
Db 765 GTTGTATTGGCGGCACATCAAGCAGCGGCATCGTGTGGAGTTTCTCTGCTGCT 824
QY 209 uLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLe 229
Db 825 CTTCTCCCTGACCCAGTTCCAGGTGTGTGAGCTGTGGCTTACCTGGCCCTCGCCGCACT 884
QY 229 uSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAs 249
Db 885 CTCAGCCACCATCAGTTTCGGCATCTACAAGTCTGTTTTACAAAGCAGTGCAGAAACCGA 944
QY 249 pGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVa 269
Db 945 CCAAGGCCACCTTTCAAGCCCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGAT 1004
QY 269 lGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgAr 289
Db 1005 TCAGAAGTACAGGACTGCTGCAGTTCTACGTGAACAGCACACTTAAGAACTGAGGAG 1064
QY 289 gLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPh 309
Db 1065 GCTCTTCCTTGTCCAGGACCTGGTGATTCCTTAAATTTGCAGTCTCTGATGTGGTCTCT 1124
QY 309 eThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLe 329
Db 1125 GACCTACGTTGGGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1184
QY 329 uPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLe 349
Db 1185 GTTTACTTACTCTAGTGTATGTTAAGCACCAGGACACAGATTTGACCAATATCTGGACT 1244
QY 349 uAlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLy 369
Db 1245 TGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCAGGCGCTAA 1304
QY 369 sArgLysAlaGlu 373
Db 1305 GAGGCACGCTGAG 1317

RESULT 6
US-09-949-016-1127
; Sequence 1127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1127
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1127
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Alignment Scores:
Pred. No.: 2,57e-42 Length: 3202
Score: 747.50 Matches: 180
Percent Similarity: 54.12% Conservative: 50
Best Local Similarity: 42.35% Mismatches: 113
Query Match: 39.14% Indels: 83
DB: 4 Gaps: 10

US-09-544-776-2 (1-373) x US-09-949-016-1127 (1-3202)
QY 4 LeuAspGlnSerProLeuValSerSerAspSerProProArgProGlnProAlaPhe 23
Db 1260 CTGGCCGACAGCCCGAGGTCAAGGCCAGGTCCGGACCGCCCAACC----- 1304
QY 24 LysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGlu 43
Db 1305 -----ATCCCCAGCCCCCTGGACCAAGAGCCGAGCGGAGTTCGGGGGAC 1352
QY 44 AspGluAspGluAspLeuGluGluValLeuGluArgLysProAlaAlaGlyLeu 63
Db 1353 -----TCAGATGTCAGCTGTGTCCGAGGACCCCATGCGCGGGAG 1394
QY 64 SerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsn 83
Db 1395 GACGCGCTGCC-----TCAGGCTATGTGAGCTTTGGCCAC 1430
QY 84 AspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal----- 100
Db 1431 GTGGGCGGCCGCCGCCCTCG-----CCGCGCTCGCCATCCATCCAGTACAGC 1478
QY 101 -----AlaProGluArgGln-ProSerTrpAspProSerProValSerThrVal-- 117
Db 1479 ATCCTGAGGAGGAGCGCGGCGCGAGCTGGACGCGAGCTCATCATCGAGTCGTCGAC 1538
QY 118 -----Pr 118
Db 1539 GCCTCTCGGCTCGGAGGAGAGCCCAAGCGGAGCAGACTCACCCCGCATGAAGCC 1598
QY 118 oAlaPro-----SerPheLeuSerAl 125
Db 1599 AGCGCCCTGGATGCCATCCGGGAGGAGACTGCGCTCGGGCCGAGAGCGTGGCCCAAGC 1658
QY 125 aAlaAlaValSerProSerLysLeuProGluAspAspGluProProAlaAarProPr 145
Db 1659 CGCGGGGCTGGCCGAGCGCGGTTCTTCCTC-GACTACCCCTCACTAGGCCCGCAGCC 1717
QY 145 oPro-----ProProAlaSerValSerProGlnAlaGluProValTrpThrProPr 162
Db 1718 TGGCCCGGAGCTGCCCTCGGAGCAGCGCCCTGGAGCCTGAGAGCCCATGTCACAGC 1777
QY 162 oAlaPro---AlaProAlaAlaProProSerThrProAlaAlaProLysArgGlySe 181
Db 1778 GAAGCTGAGAGACTCGAGTTCACAAAGTCTCGGGCCACAAAGGGCCCTGGGCC 1837
QY 181 rSerGly-----SerValValValAspLeu 189
Db 1838 TCTAGTCTCGGGCCGCCCCCACTGCTGTTTCTCAATAAGCAAAAGCTATTGACCT 1897
QY 189 uLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLe 209
Db 1898 GTTGTATTGGCGGCACATCAAGCAGCGGCATCGTGTGGAGTTTCTCTGCTGCT 1957
QY 209 uLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLe 229
Db 1958 CTTCTCCCTGACCCAGTTCCAGGTGTGTGAGCTGTGGCTTACCTGGCCCTCGCCGCACT 2017
QY 229 uSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAs 249
Db 2018 CTCAGCCACCATCAGTTTCGGCATCTACAAGTCTGTTTTACAAAGCAGTGCAGAAACCGA 2077
QY 249 pGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVa 269
Db 2078 CGAAGGCCACCTTTCAAGGGCCCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGAT 2137
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QY 269 lGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThrIleLysGluLeuArgAr 289
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2138 TCAGAGTACAGCGACTGCGCTGCGAGTCTACGTGAACAGCACACTTAAGGAACTGAGGAG 2197
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 289 gLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValph 309
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2198 GCTCTTCCTTGTCCAGAGCTGGTGGATTCTTAAAAATTTGCAGTCTGATGTGGCTCCT 2257
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 309 eThrTyrValGlyAlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLe 329
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2258 GACCTAGTTGGCGCTCTCTTCAATGGCCTGACCTGCTGCTCATGGCTGTGGTTCCAT 2317
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 329 uPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLe 349
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2318 GTTACTCTACCTGTAGTGTATGTTAAGCACCGACGACAGTATGACCAATATCTGGGACT 2377
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 349 uAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLy 369
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2378 TGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAAAATCCAGGCGCTAA 2437
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QY 369 sArgLysAlaGlu 373
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2438 GAGCAGCGCTGAG 2450
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RESULT 7
US-09-149-476-254
; Sequence 254, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PC/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
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Db	596	ATTGCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCTTGAACCTGGCTGTCTTCAATGCG	655	EARLIER FILING DATE: 1997-05-23
Qy	308	valPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuileLeuAlaLeuile	327	EARLIER APPLICATION NUMBER: 60/047,598
Db	656	CTGATCACCCTATGTTGGTGTCTGTTTTTAACGGAATCACCCCTTCTAATTCTTGGTGAAC	715	EARLIER FILING DATE: 1997-05-23
Qy	328	SerLeuPheSerValProValIleTyrGluAtrGHisGlnAlaGlnIleAspHisTyrLeu	347	EARLIER APPLICATION NUMBER: 60/047,613
Db	716	CTCATTTTCAGTGTCCGATTTGTTCTATGAGAAGTACAAGACCCAGATTCATCATCTTT	775	EARLIER FILING DATE: 1997-05-23
Qy	348	GlyLeuAlaAsnLysAenValIysAspAlaMetAlaValIleGlnAlaValIleProGly	367	EARLIER APPLICATION NUMBER: 60/047,612
Db	776	GGCATGCCCGAGATCAGACCAGTCATTTGTGAAAGATTCACAGCAAACTCCCTCGA	835	EARLIER FILING DATE: 1997-05-23
Qy	368	Leu---LysArgIysAlaGlu	373	EARLIER APPLICATION NUMBER: 60/047,632
Db	836	ATCGCCAAAAMAAAGGCAGAA	856	EARLIER FILING DATE: 1997-05-23
RESULT 8				EARLIER APPLICATION NUMBER: 60/043,568
US-09-149-476-255				EARLIER FILING DATE: 1997-04-11
; Sequence 255, Application US/09149476				EARLIER APPLICATION NUMBER: 60/043,314
; Patent No. 6420526				EARLIER FILING DATE: 1997-04-11
; GENERAL INFORMATION:				EARLIER APPLICATION NUMBER: 60/043,569
; APPLICANT: Rosen et al.				EARLIER FILING DATE: 1997-04-11
; TITLE OF INVENTION: 186 Human Secreted proteins				EARLIER APPLICATION NUMBER: 60/043,311
; FILE REFERENCE: P2002P1				EARLIER FILING DATE: 1997-04-11
; CURRENT APPLICATION NUMBER: US/09/149,476				EARLIER APPLICATION NUMBER: 60/043,671
; CURRENT FILING DATE: 1998-09-08				EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: PCT/US98/04493				EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1998-03-06				EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/040,162				EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-03-07				EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/040,333				EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-03-07				EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/038,621				EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-03-07				EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER APPLICATION NUMBER: 60/040,626				EARLIER FILING DATE: 1997-04-11
; EARLIER FILING DATE: 1997-03-07				EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER APPLICATION NUMBER: 60/040,334				EARLIER FILING DATE: 1997-04-11
; EARLIER FILING DATE: 1997-03-07				EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER APPLICATION NUMBER: 60/040,336				EARLIER FILING DATE: 1997-06-06
; EARLIER FILING DATE: 1997-03-07				EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER APPLICATION NUMBER: 60/040,163				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-03-07				EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER APPLICATION NUMBER: 60/047,600				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER APPLICATION NUMBER: 60/047,615				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER APPLICATION NUMBER: 60/047,597				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER APPLICATION NUMBER: 60/047,502				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER APPLICATION NUMBER: 60/047,633				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER APPLICATION NUMBER: 60/047,583				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER APPLICATION NUMBER: 60/047,617				EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-05-23				

/ EARLIER APPLICATION NUMBER: 60/056,636  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,874  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,910  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,864  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,631  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,845  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,892  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/057,761  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/057,588  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,595  
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 / EARLIER APPLICATION NUMBER: 60/047,599  
 / EARLIER FILING DATE: 1997-05-23  
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 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,908  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/048,964  
 / EARLIER FILING DATE: 1997-06-06  
 / EARLIER APPLICATION NUMBER: 60/057,650  
 / EARLIER FILING DATE: 1997-09-05  
 / EARLIER APPLICATION NUMBER: 60/056,884  
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 / EARLIER FILING DATE: 1997-09-05  
 / EARLIER APPLICATION NUMBER: 60/049,610  
 / EARLIER FILING DATE: 1997-06-13  
 / EARLIER APPLICATION NUMBER: 60/061,060

/ EARLIER FILING DATE: 1997-10-02  
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 QY 62 GlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAspPhe 81  
 DB 50 GGATTATTCTATTTCGCC----- 67  
 QY 82 GlyAsnAspPheValProAlaProArgGlyPheLeuProAlaAlaProPro----- 99  
 DB 68 -----TCCCTCTCTCCCGCCCGTATCTTTTACCCCTTCTCCACCCCTCGCTCG 118  
 QY 100 -----ValAlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVal 117  
 DB 119 CGTASCATGGCGAGCGTGGCGGCA-----CTCAGTCCCAT 157  
 QY 118 ProAlaProSerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAsp 137  
 DB 158 CCATCTCCT----- 166  
 QY 138 GluProProAlaArgProProProProProAlaSerValSerProGlnAlaGluPro 157  
 DB 167 CQTCTCTCTTCGGAGCCGCGCGCGCGCGGCGGCGGAGCCAG---GAGCCT 223  
 QY 158 ValTrpThrProAlaProAlaProAlaProAlaProSerThrProAlaAlaProLys 177  
 DB 224 -----GCCCGCGCC-----TGGGACGA 241  
 QY 178 ArgArgGlySerSerGlySerValValValAspLeuLeuTrpTrpArgAspIleLysLys 197  
 DB 242 AGAGCTGC-AGCTCCTCTCTGCGGTGCACGATCTGATTTCTGGAGAGATGTGAGAAG 300  
 QY 198 ThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIle 217  
 DB 301 ACTGGGTTGTCTTTGGCACCACCGTGCATGCTCTTCTCCCTGGCAGCTTTCAGTGTC 360  
 QY 218 ValSerValThrAlaTyrlleAlaAlaLeuLeuSerValThrIleSerProArgIle 237  
 DB 361 ATCAGTGTGTTTCTTACCTCATCTGGCTCTTCTCTGTCCACCATCAGTTCAGGATC 420  
 QY 238 TyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 257  
 DB 421 TACAAGTCGTTCATCCAAGCTGACAGAAGTCAAGAAGGAGGCGCATCCATTCAGAGCTAC 480  
 QY 258 LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu 277  
 DB 481 CTGGAGCTAGACATTACTCTGTCTCAGAAAGTTCCTCATTAATACATGAATGTCATG 540  
 QY 278 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuVal 297  
 DB 541 GTGCACATCAACAGGCGCCCTGAACCTCATTTATTCGTCTCTTTCTGGTAGAAGATCTGGTT 600  
 QY 298 AspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 317  
 DB 601 GACTCCTTGAAGCTGGCTGTCTTCATGTGGCTGATGACCTATGTGGTGTCTGTTTAAAC 660  
 QY 318 GlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGlu 337  
 DB 661 GGAATCACCCCTCTTAATTTCTGCTGAATGCTATTTTCAGTGTCCGATGCTCTATGAG 720  
 QY 338 ArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAlaAsnLysAsnValLysAspAla 357

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Db 721 AAGTACCAAGCCAGATGATCACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATT 780
Qy 358 MetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu 373
Db 781 GTTGAAGAAGTCCAGCAAACTCCCTGGAAATGCCCAAAAAAAGGCAGAA 831

RESULT 9
US-09-949-016-2988
; Sequence 2988, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2988
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2988

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Score: 613.50 Matches: 114
Percent Similarity: 80.42% Conservative: 38
Best Local Similarity: 60.32% Mismatches: 36
Query Match: 32.12% Indels: 1
DB: 4 Gaps: 1

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Qy 206 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 225
Db 70 CTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGCATCATGCTGTTCTTACCTCATC 129
Qy 226 LeuAlaLeuSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIle 245
Db 130 CTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCTGTA 189
Qy 246 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 265
Db 190 CAGAAGTCAGAGAAGGCCATCCATCAAGCCCTACCTGACGCTAGACATTAATCTGTGCC 249
Qy 266 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
Db 250 TCAGAAGCTTTCCATTAATACATGATGCTGCCATCATCATCAACAGGGCCCTGAAA 309
Qy 286 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 305
Db 310 CTCATTATTCGTCTCTTTCTGTGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGCTTC 369
Qy 306 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 325
Db 370 ATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGAATCACCTCTTAATCTTGTCT 429
Qy 326 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 345
Db 430 GAACTGCTCATTTTCAGTGCTCCGATTTGCTATGAGAAGTACCAAGACCCAGATGATCAC 489
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Qy 346 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 365
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Qy 366 ProGlyLeu---LysArgLysAlaGlu 373
Db 550 CCTGGAATCGCCAAAAAAGGCAGAA 576

RESULT 10
US-08-700-607-4
; Sequence 4, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOBI
; CLONE: 31870
US-08-700-607-4

Alignment Scores:
Pred. No.: 2,756-29 Length: 1095
Score: 550.00 Matches: 131
Percent Similarity: 58.78% Conservative: 43
Best Local Similarity: 44.26% Mismatches: 74
Query Match: 28.80% Indels: 49
DB: 2 Gaps: 7

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Db 3475 TGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAG 3514

## RESULT 12

US-09-149-476-102  
; Sequence 102, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
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; EARLIER APPLICATION NUMBER: 60/047,595
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Pred. No.:	6,97e-29	Length:	794
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Best Local Similarity:	41.77%	Mismatches:	77
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DB:	3	Gaps:	8

US-09-544-776-2 (1-373) x US-09-149-476-102 (1-794)

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DB 45 TTATTCTATTTCCTCC-----
QY 83 AsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProPro----- 99
DB 60 -----TCCCTCTCTCCCGCCCGATATCTCTTTTTCACCCCTTCTCCACCCCTCGCTCGCGT 113
QY 100 ----ValAlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValPro 118
DB 114 ACCATGGCGAGCGTCGGCGCA-----CTCAGTCCCATTTCCA 152
QY 119 AlaProSerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGlu 138
DB 153 TCTCT-----CGT 161
QY 139 ProProAlaArgProProProProAlaSerValSerProGlnAlaGluProVal 158
DB 162 CGTCTTCGGAGCGCGCGTCCGCGCGCGGGCGGAGCCAG--GAGCCT-- 215
QY 159 TrpThrProProAlaProAlaProAlaProProSerThrProAlaProLysValArg 178
DB 216 -----GCCCGCCC-----TGGGACGCAAGA 236
QY 179 ArgGlySerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThr 198
DB 237 GCTGC-AGCTCTCTCTGCGGTGACGATCTGATTTCTGGAGATGTGAGAGACT 295
QY 199 GlyValValPheGlyAlaSerLeuLeuLeuLeuSerLeuThrValPheSerIleVal 218
DB 296 GGGTTTGTCTTTGGAC--ACGCTGATCATGCTGCTTCTCCCTGGCAGCTTTAGTGTCTATC 353
QY 219 SerVal-ThrAlaTyrIleAlaLeuLeuLeuSerValThrIleSerProArgIleTy 238
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DB 414 CAAGTCGCTCATCCAGCTGTWCAGANTCAGAAAGGCCATCCANTCCAAAGCCTACC 473
QY 258 euGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuG 278
DB 474 TGGACGTAGACATTACTCTGCTCTCAGAGCTTTCATAAATTACATGAATGCTGCCATGG 533
QY 278 lyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValA 298
DB 534 TGCACATCAACAGGCGCCCTGAAACTCATTTTCGTCCTCTTCTGGTAGAAGATCTGGTTG 593
QY 298 spSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnG 318
DB 594 ACTCTTGAAGCTGGCTGCTTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACG 653
QY 318 lyLeuThrLeuLeuLeuAlaLeuLeuLeuSerLeuPheSerValProValIleTyrGluA 338
DB 654 GAATCACCTTCTTAATTCTTGTGTAAGTCTCATTTTTCAGTGTCCCGATTGCTATGAGA 713
QY 338 rgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaM 358
DB 714 AGTACAAGACCCAGGATTTGATCTACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTG 773
QY 358 etAlaLysIleGlnAlaLys 364
DB 774 TTGAAGAAGATCCCAAGCAAA 793

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RESULT 13

US-09-949-016-1419  
; Sequence 1419, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTNER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307



CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIORITY APPLICATION NUMBER: 60/241,755  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY APPLICATION NUMBER: 60/237,768  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY APPLICATION NUMBER: 60/231,498  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 1419  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1419

Alignment Scores:  
Pred. No.: 2,44e-27 Length: 2181  
Score: 527.50 Matches: 149  
Percent Similarity: 43.74% Conservative: 57  
Best Local Similarity: 31.63% Mismatches: 140  
Query Match: 27.62% Indels: 125  
DB: 4 Gaps: 15

US-09-544-776-2 (1-373) x US-09-949-016-1419 (1-2181)

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QY 17 ProArgProGlnProAlaPheLysTyrGlnPheValArgGluProGluAspGluGlu 36
DB 385 CCGCGCCCGCAGGCGC-----CGTCTAGTCTCGAACCACGAGAC-----423
QY 37 GluGluGluGluGluGluGluAspGluAspGluAspGluGluGluValLeuGlu 56
DB 424 -----CAGCACCTCAGCCAGCCTGGCGGCACAGCTTGGAGAGCATCCCGAGCTGAGC 477
QY 57 ArgLysProAlaAlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAla 76
DB 478 CAATCCCGGAGCGCTGAGCAGCGGGGTGATCTT---GACACCGCGCTCCATCCGAGCGC 534
QY 77 ProLeuMetAspPheGly-----82
DB 535 CCTCTGAGAGACCTGAGGCTTCGGTTGGACCATCTGGCTGGGTCGGCCGGGAGACGGGA 594
QY 83 -----AsnAspPheValProProAla 89
DB 595 TCGGGGAGGACTCTTCCACGAGCAGCTCCACCCCGCTGGAAGACGAAGAACCCCAAGAA 654
QY 90 ProArgGlyPhe-----LeuProAlaAla 97
DB 655 CCAACAGATTGGAGACAGAGAGAGCTGGGGAAGAACTGGACCTACGACTCCGACTTGTCT 714
QY 98 ProProValAlaProGlu---ArgGlnProSerTrpAspPro-----SerProVal 113
DB 715 CAGCCCTCATCGCCCGGAGGTCTTGACTCCCGAGCTCAGTCCGGGCTCTGGGACACCCAG 774
QY 114 SerSerThrValProAlaProSerPheLeuSerAlaAlaValSerProSerLys---132
DB 775 GCGCGTACT---CGTCCCATCCCGATCCGAGATTCGAATCTCTGGCCCGGAAGAGCCA 831
QY 133 LeuProGluAspGluProProAlaAlaArgProProProProAla-----149
DB 832 TTGCTGGAAGAGAGAAAGCAGTGGGGGCCACTGGAGCGAGCGCCAGTAAAGGGGACAG 891
QY 150 -----SerValSerProGln-----154
DB 892 TGCTCGATAGCAGGACCAATTAGATTACCGGTGGAGCCAGCTTCTTAGGAACAGCT 951
QY 154 -----154
DB 952 ATGAATGTTAAAGACATCAATTGCTTTTGGCTGTTTACAAGACGGTTCCAAATTTGGAA 1011
QY 155 ---AlaGluProValTrpThr-----ProProAlaProAla 165
DB 1012 TTGTCCCACTCTGTGGACAGCCATTGGCTGGGTCCAAAGGGGGCCCCACCCCTTACT 1071
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QY 166 Pro-----AlaAlaProSerThrProAlaAlaProLys 177
DB 1072 CCTGCTCCGGGTTCTACTGAAGTGGCAAAATCCCGAAGACGAGCGGTGTCCTCCAGC 1131
QY 178 ArgArg-----GlySerSerGlySerValValAlaSerLeuTyrTrpArgAspIle 195
DB 1132 CTCTCACTCGGAGCCGATATGGGGAGTAAGTGGGACCTGTCTACTGGAAGGACAGC 1191
QY 196 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 215
DB 1192 AGGACGTGAGAGTGTCTTTCAGGCGCTGATGGTCTCTCTCTCTCTCTCTCTCTCTCTC 1251
QY 216 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPro 235
DB 1252 AGCATCGTGTCCGTGGCGGCACTTGGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTC 1311
QY 236 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 255
DB 1312 AGGGTTTACCGCAAGTGTCTGAGCGGCTGCACCGGGGGATGGAGCAACCTTTTCCAG 1371
QY 256 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 275
DB 1372 GCCTACTGATGTGACCTCACCCTGACTCGGAGCAGACGAGCGTTGTCTCCACAG 1431
QY 276 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspAsp 295
DB 1432 ATCACCTCCCGCTGTCTCGGCGGCCACGACGCTCGGCACTTCTCTCTGTAGAGAC 1491
QY 296 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrValGlyAlaLeu 315
DB 1492 CTGCTGGATTCCTCAAGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 1551
QY 316 PheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIle 335
DB 1552 TTCAATGGTTTGACTCTTCTCATCTCGGAGTGTGGTCTATTCACCATCCCTCTGCTG 1611
QY 336 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAlaSerValLys 355
DB 1612 TACCGGACGACCCAGGCTCAGATCGACCAATATGTGGGTGGTGACCAATCAGTTGAGC 1671
QY 356 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu-----368
DB 1672 CACATCAAGCTAAGATCCGAGTAAATCCCGGAGACCGGAGCCCTTGCGCTCTGACGA 1731
QY 369 -----LysArgLysAlaGlu 373
DB 1732 GCGGAGTCTCCGATCCAAAGCCAAAGCCGAA 1764
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## RESULT 14

US-09-270-767-13561  
Sequence 13561, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13561  
LENGTH: 2014  
TYPE: DNA  
ORGANISM: *Drosophila melanogaster*  
US-09-270-767-13561

Alignment Scores:  
Pred. No.: 2,2e-26 Length: 2014  
Score: 513.00 Matches: 96  
Percent Similarity: 71.79% Conservative: 44  
Best Local Similarity: 49.23% Mismatches: 55  
Query Match: 26.86% Indels: 0

DB:	4	Gaps:	0
US-09-544-776-2 (1-373) x US-09-270-767-13561 (1-2014)			
Qy	179	AtqGlySerSerGlySerValValAspLeuLeuTyrTrpAqAspIleLeuLysLysThr	198
Db	134	CGAAATGTCGAACAGATTGTTGAATCCCTTATCTACTGGCGCGATGTGAAGAATCC	193
Qy	199	GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal	218
Db	194	GGCAVTTGCTTCGGCGCTGGCTGATCACATGCGCGCCATCTCCAGCTTCTCGGTGATC	253
Qy	219	SerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyr	238
Db	254	AGCGTGTTCGCCCTACTCTGCGCTCTTAACCTCTTCGGCACCGCGCTTCAGAATCTAC	313
Qy	239	LysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeu	258
Db	314	AAATCTGTGACACAGCGCTGCNAAGACAAACGAGGGTCACCCCTTTAGGATTACCTG	373
Qy	259	GluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly	278
Db	374	GAGCTGGATCTCAGCTGCTGCGCACGAAAGGTACAGAACATTGCGCGGTGGCTGTGGCA	433
Qy	279	HisValAsnCyseThrIleLysGluLeuArgGluPheLeuAlaAspLeuValAsp	298
Db	434	CATATCAATGGGTTCAATCCGAGCTGAGGGCTGTGTTCTTGTTGAGGATATCATCGAT	493
Qy	299	SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly	318
Db	494	TCGATCAAGTTCGGCGTCATTCTGTGGGTCTTCACTACGTGGGTGCTGCTTTCAATGGC	553
Qy	319	LeuThrLeuLeuIleAlaLeuLleSerLeuPheSerValProValIleTyrGluArg	338
Db	554	ATGACTCTGGTCATCTTGGCCCTTTGTCTCGCTGTTTACCTTGGCCCAAGGTCTACGAGA	613
Qy	339	HisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet	358
Db	614	AACAGCAATCGATCGACACTCACTTGGATCTGGTGGCGAGCAAAATGACAGAAATCACC	673
Qy	359	AlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu	373
Db	674	GACAGATCCGAGTGGCATCCCATTTGGCAACAGAAGCCCGAG	718

RESULT 15

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US-09-513-999C-2227
; Sequence 2227, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2227
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 236..439
US-09-513-999C-2227

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Alignment Scores:	
Pred. No.:	8.77e-16
Score:	347.00
Length:	441
Matches:	68

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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 18.17%              Indels: 0
DB: 4                             Gaps: 0

US-09-544-776-2 (1-373) x US-09-513-999C-2227 (1-441)

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Db      236  ATGGAGACCTGGACAGTCCTCTGCTCTGCTCGGACAGCCACCCCGCCGCGAG 2395
Qy      21  ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
Db      296  CCGGGGTTCAGTACCACTTCGTGAGGAGGCCCGAGGAGGAGGAGGAGGAGGAG 3555
Qy      41  GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
Db      356  GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGCTGCTGGAGAGAGCCCGCC 415
Qy      61  AlaGlyLeuSerAlaAlaProVal 68
Db      416  GCCGGGCTGTCGCGGCCCCAGTG 439

Search completed: August 3, 2005, 23:15:46
Job time : 224 secs

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Search completed: August 3, 2005, 23:15:46  
Job time : 224 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:14:22 ; Search time 4328 Seconds  
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4176.016 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLSDPLVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRKAE 373

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	3.6	48	6	AR199544 Sequence
2	68	3.6	48	6	AR374696 Sequence
3	68	3.6	48	6	AR409331 Sequence
4	68	3.6	48	6	AX239593 Sequence

5	68	3.6	48	6	BD056458	Novel low
6	66	3.5	48	6	AR178317	Sequence
7	66	3.5	48	6	AX323399	Sequence
8	66	3.5	50	6	AS1711	Sequence 17
9	66	3.5	50	6	AR167590	Sequence
10	66	3.5	50	6	AR178300	Sequence
11	66	3.5	50	6	AX323382	Sequence
12	66	3.5	50	6	AX686852	Sequence
13	63	3.3	50	6	AR356035	Sequence
14	63	3.3	50	6	AR537591	Sequence
15	60	3.1	50	6	AR232180	Sequence
16	60	3.1	50	6	AX539582	Sequence
17	60	3.1	50	6	AX539583	Sequence
18	59	3.1	45	6	AR199538	Sequence
19	59	3.1	45	6	AR374690	Sequence
20	59	3.1	45	6	AR409325	Sequence
21	59	3.1	45	6	AX239587	Sequence
22	59	3.1	45	6	BD056452	Novel low
23	58	3.0	34	6	BD169737	Sequence
24	58	3.0	38	6	BD169738	Sequence 1
25	58	3.0	40	6	BD169738	C-terminu
26	57	3.0	39	6	BD169738	Sequence 9
27	57	3.0	42	6	BD247090	Improved
28	57	3.0	47	6	AX539586	Sequence
29	57	3.0	47	6	AX539587	Sequence
30	57	3.0	48	6	AR178317	Sequence
31	57	3.0	48	6	AR306664	Sequence
32	57	3.0	48	6	AR340099	Sequence
33	57	3.0	48	6	AR412168	Sequence
34	57	3.0	48	6	AX323399	Sequence 17
35	57	3.0	50	6	AS1711	Sequence 17
36	57	3.0	50	6	AR167590	Sequence
37	57	3.0	50	6	AR178300	Sequence
38	57	3.0	50	6	AX323382	Sequence
39	57	3.0	50	6	AX686852	Sequence
40	56	2.9	42	6	AX512498	Sequence
41	56	2.9	42	6	AX573414	Sequence
42	56	2.9	42	6	AX746300	Sequence
43	56	2.9	48	6	AR306674	Sequence
44	56	2.9	48	6	AR340109	Sequence
45	56	2.9	48	6	AR412178	Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS AR199544 48 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 36 from patent US 6355451.  
ACCESSION AR199544  
VERSION AR199544.1 GI:20249618  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 36 12-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..48  
/organism="unknown"  
/mol\_type="unassigned DNA"

#### ORIGIN

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Best Local Similarity: 68.75% Mismatches: 0  
Query Match: 3.56% Indels: 0  
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US-09-544-776-2 (1-373) x AR199544 (1-48)

[illegible]

RESULT 2			
AR374696			
LOCUS	AR374696	48 bp	DNA
DEFINITION	Sequence 36 from patent US 6605588.	linear	PAT 18-DEC-2003

VERSION	AR374696.1	GI:40077511
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	
REFERENCE	1 (bases 1 to 48)	
AUTHORS	Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.	
TITLE	Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis	
JOURNAL	Patent: US 6605598-A 36 12-AUG-2003;	

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FEATURES
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      1. .48
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## ORIGIN

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Pred. No.:	3.39e+04
Score:	68.00
Percent Similarity:	100.00%
Best Local Similarity:	68.75%
Query Match:	3.56%
DB:	6
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 5
	Matches: 11
	Length: 48

US-09-544-776-2 (1-373) x AR374696 (1-48)

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Qy      33 AspGluGluGluGluGluGluGluGluGluGluGluGluGluGluAspGluAsp    48  
       :::::::::::::::::::::::::::::  
Db      1 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCAGCACGCAC    48
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RESULT 3			
AR409331	AR409331	48 bp	DNA
LOCUS	Sequence 36	from patent	US 6632923.
DEFINITION		linear	PAT 18-DEC-2003

AR409331.1 GI:40160119

ORGANISM	SOURCE	Unknown.	Unknown.	Unknown.	Unclassified.

**AUTHORS** Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
**TITLE** Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
**JOURNAL** Patent: US 6632923-A 36 14-OCT-2003:

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FEATURES
  Location/Qualifiers
    1..48
      /organism="unknown"
      /mol_type="genomic DNA"

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## ORIGIN

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Alignment Scores:
Pred. No.: 3.39e+04
Score: 68.00
Percent Similarity: 100.00%
Best Local Similarity: 68.75%
Query Match: 3.56%
DB: 6
Length: 48
Matches: 11
Conservative: 0
Mismatch: 5
Indels: 0
Gaps: 0

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US-09-544-776-2 (1-373) x AR409331 (1-48)

[illegible]

RESULT 4	AX239593	LOCUS	AX239593	SEQUENCE 16	FROM PATENT	WO0164874
						48 bp

AX239593  
AX239593.1 GI:15797  
Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1

**AUTHORS** Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
**TITLE** Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis  
**JOURNAL** Patent: WO 0164874-A 36 07-SEP-2001; Boston Heart Foundation, Inc. (US)

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FEATURES
source
1. 48
Location/Qualifiers
Boston Heart Foundation, Inc. (50)
/organism="Homo sapiens"
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## ORIGIN

Alignment Scores:	
Pred. NO.:	3.39e+04
Score:	68.00
Percent Similarity:	100.00%
Best Local Similarity:	68.75%
Query Match:	3.56%
DB:	6
Length:	48
Matches:	11
Conservative:	5
Mismatches:	0
Indels:	0
Gaps:	0

US-09-544-776-2 (1-373) x AX239593 (1-48)

[illegible]

RESULT 5	BD056458	LOCUS	BD056458	48 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis..						

ACCESSION  
BD056458

KEYWORDS  
SOURCE JP 2001506983-A/16.  
ORGANISM Aequorea victoria  
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae; Aequoreidae; Aequorea.

REFERENCE 1 (bases 1 to 48)  
 LEES, A.M., LEES, R.S., LAW, S.W. and ARJONA, A.A.  
 TITLE Novel low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 JOURNAL Patent: JP 200106983-A 16 29-MAY-2001;

BOSTON HEART FOUNDATION

PD 29-MAY-2001  
PF 26-NOV-1997 JP 1998524870  
PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PT  
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC  
C07H21/00,

PC	C07K7/00, C07K34/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566	CC
Strandedness: Single;		
CC Topology: Linear;		
EH	Key	Location/Qualifiers.
FEATURES		
source	Location/Qualifiers	
		1..48



[illegible]

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Job time : 4331 secs

Search completed: August 4, 2005, 01:02:09  
Job time : 4331 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:14:22 ; Search time 560 Seconds  
(without alignments)  
3942.971 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLDSPVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRAE 373

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=p2nslm50.rng -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=50 -USER=US09544776@cgn.1.1.708@runat\_03082005\_181413\_27611 -NCFU=6  
-ICPU=3 -NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	3.6	48	5	Aah26508
2	66	3.5	48	6	Aas21106 (GGA)16 D
3	66	3.5	50	2	Aat32776 Homopurin
4	66	3.4	50	6	Aas19342 Plasmid X
5	64	3.4	42	10	Abz22128 Polyanion

64	3.4	42	10	Abz222092
64	3.4	45	4	Aai64451 SSR motif
64	3.4	50	10	Adc56858 Micro gol
64	3.4	50	10	Adc56859 Micro gol
63	3.3	50	2	Aav76464 Staphyloc
60	3.1	50	6	Abse67031 Human MRP
60	3.1	50	6	Abse67032 Human MRP
60	3.1	50	8	Abx13592 Human ser
60	3.1	50	10	Aad60995 Human ser
60	3.1	50	12	Adh59088 Human KSE
59	3.1	42	4	Aas13776 Simple se
59	3.1	42	4	Aas13779 Simple se
59	3.1	45	5	Aah26502 Low densi
58	3.0	34	6	Abk95216 PCR prime
58	3.0	38	2	Aat06967 Primer fo
58	3.0	40	6	Abk95217 PCR prime
57	3.0	39	12	Adk61703 Base cont
57	3.0	47	6	Abse67036 Human MRP
57	3.0	47	6	Abse67035 Human MRP
57	3.0	48	2	Aax27671 [GPPP]n 1
57	3.0	48	6	Aas21106 (GGA)16 D
57	3.0	48	6	AbL51775 Hydroxypr
57	3.0	50	2	Aat32776 Homopurin
57	3.0	50	6	Aas19342 Plasmid X
56	2.9	42	4	Aah48668 Anti-trop
56	2.9	42	5	Aah21345 CSC-F ove
56	2.9	42	8	Abz21455 Chicken i
56	2.9	43	2	AaQ81075 supF gene
56	2.9	43	2	AaQ81075 supF gene
56	2.9	48	2	Aax70014 Triplex-f
56	2.9	48	2	Aax27675 Potato le
56	2.9	48	6	Aas16547 Ligatation
56	2.9	48	6	AbL51785 Hydroxypr
56	2.9	50	10	ADD31857 Synthetic
55	2.9	45	2	Aav55838 Sequence
55	2.9	37	2	AaQ05014 Sequence
55	2.9	37	2	AaQ36334 HSPOL2pa
55	2.9	37	2	AaQ36335 HSPOL2an
55	2.9	38	6	Abse67040 Human MRP
55	2.9	38	6	Abse67039 Human MRP
55	2.9	40	3	Aaz96053 Polynucle

ALIGNMENTS

RESULT 1

Aah26508  
ID Aah26508 standard; DNA; 48 BP.

XX Aah26508;

DT 12-NOV-2001 (first entry)

DE Low density lipoprotein binding protein (LBP) polynucleotide.

XX Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;  
KW antiarteriosclerotic; therapy; diagnosis; vaccine; ss.

OS Mammalia.

PN WO200164874-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006356.

PR 02-MAR-2000; 2000US-00517849.

PR 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

XX Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.



CC acids, proteins, endotoxins, nucleases, etc. by passing the mixture over  
 CC a support to which an oligonucleotide is covalently attached; the  
 CC oligonucleotide is able to form a triple helix by hybridisation with a  
 CC specific sequence present in the dsDNA. The present sequence is a  
 CC preferred homopurine target for triplex formation with a single-stranded  
 CC oligonucleotide. The target sequence may be present naturally, e.g. in a  
 CC plasmid origin of replication, or can be introduced artificially. The  
 CC method is particularly suited to purification of plasmid DNA

XX Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5.27e+04 Length: 50  
 Score: 66.00 Matches: 12  
 Percent Similarity: 100.00% Conservatives: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 3.46% Indels: 0  
 DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAT32776 (1-50)

QY 32 GluAspGluGluGluGluGluGluGluGluGluGluAspGluAsp 46  
 AAS19342  
 DB 4 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 48

RESULT 4  
 AAS19342  
 ID AAS19342 standard; DNA; 50 BP.

AC AAS19342;

XX 20-MAR-2002 (first entry)

DT Plasmid XL2725 sequence.

DE ds; DNA purification; triple helix; plasmid purification; XL27255.

XX Synthetic.

OS Key Location/Qualifiers

FH repeat\_region 6..50

FT /\*tag= a

FT /rpt\_type= TANDEM

FT repeat\_unit 6..8

FT /\*tag= b

FT /note= "GCA repeat type"

XX WO200192511-A2.

PN 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US017122.

PF 26-MAY-2000; 2000US-00580923.

PR (AVET ) AVENTIS PHARMA SA.

XX Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;

XX WPI; 2002-097772/13.

XX Purifying double-stranded (ds) DNA from a solution containing dsDNA and

XX other components, comprises passing the solution through a support

XX comprising a covalently coupled oligonucleotide able to form a triple

XX helix with the dsDNA.

XX Example 7.1; Page 20; 40pp; English.

XX This invention comprises a method of purifying double-stranded DNA from a

XX solution containing the double-stranded DNA mixed with other components,

XX comprising passing the solution through a support comprising a covalently

XX coupled oligonucleotide capable of forming a triple helix with the double

XX -stranded DNA by hybridisation with a specific sequence present in the

CC double-stranded DNA. The method is useful for purifying double-stranded  
 CC DNA contained in a solution and mixed with other components. The new  
 CC method is a simple, rapid and effective method for DNA purification, and  
 CC makes it possible to obtain especially high purities with high yields.  
 CC The method enables DNA to be purified from complex mixtures comprising  
 CC other nucleic acids, proteins, endotoxins, nucleases and the like. The  
 CC supports may be readily recycled, and the DNAs obtained display improved  
 CC properties to pharmaceutical safety. Further, the method entails only one  
 CC step contrary to prior art. The present sequence represents the sequence  
 CC of the plasmid XL2725 verified upon sequencing, this sequence differs  
 CC from the expected sequence (GGA)17

XX Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5.27e+04 Length: 50  
 Score: 66.00 Matches: 12  
 Percent Similarity: 100.00% Conservatives: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 3.46% Indels: 0  
 DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x AAS19342 (1-50)

QY 32 GluAspGluGluGluGluGluGluGluGluGluGluAspGluAsp 46  
 DB 4 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 48

RESULT 5

ABZ22128

ID ABZ22128 standard; DNA; 42 BP.

XX AC ABZ22128;

XX 11-MAR-2003 (first entry)

DT Polyanionic polymer related oligonucleotide #82.

DE Polyanionic polymer; bioactivity; water solubility; ss.

XX Synthetic.

OS WO200277036-A2.

PN 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US008614.

PF 21-MAR-2001; 2001US-0277705P.

PR (LEUN/) LEUNG D W.

XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;

XX Waggoner DW;

XX WPI; 2003-058367/05.

XX Producing monodispersed preparation of polyanionic polymer for therapy,

XX by expressing vector comprising ligation product of oligonucleotides

XX encoding glutamate/aspartate residues in host cell and isolating the

XX product.

XX Example 7; Fig 8; 74pp; English.

XX The present invention describes a method (M) for producing a

XX monodispersed preparation of a polyanionic polymer (PP) larger than 10

XX KD. (M) involves inserting into an expression vector (EV) a ligation

XX product formed by ligating together oligonucleotides that encode

XX glutamate/aspartate residues, expressing EV in a host cell, and isolating

XX the protein product (P) of EV, where (P) is PP and at least 80% of PP is

XX approximately of the same molecular weight. Also described: (1) a

XX recombinant fusion protein (I) comprising a polyanionic polypeptide and

XX another polypeptide at either one end or at both ends of it; (2) a







On 160 ThrProProAlaProAla 167

IIS-09-544-776-2 (1-373) x ARX13592 (1-50)





US-09-544-776-2 (1-373) x ADH59088 (1-50)

```
Qy 143 ProProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
Db 42 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19

Qy 163 AlaProAlaProAlaAla 168
Db 18 AGGCCCGCGCGCGCGCGCC 1
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Search completed: August 4, 2005, 01:11:41  
Job time : 563 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:14:22 ; Search time 3086 Seconds  
(without alignments)  
4600.769 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 373

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q/cgn2\_1/USPTO\_spool\_p/US09544776/runat\_03082005\_181414\_27631/app\_query.fasta\_1.519  
-DB=EST -Qfmt=fastap -SUFFIX=p2nszlm50.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50  
-USER=US09544776 @CGN 1.1 5180 @runat\_03082005\_181414\_27631 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	3.7	49	1	AA145482 mr62a06.r
c 2	70	3.7	50	9	BX976589 Forward s
c 3	68	3.6	50	9	CG731182 1119136A0
c 4	66	3.5	49	8	AZ840678 2M0138016
c 5	66	3.5	50	9	CR041958 Forward s
c 6	65	3.4	31	8	AZ861612 2M0168P16
c 7	65	3.4	48	9	AL752522 Arabidops
c 8	65	3.4	49	9	TA33D12P
c 9	65	3.4	50	9	BX002655 Arabidops

c	10	65	3.4	50	9	CR154670
c	11	64	3.4	48	8	AZ646447
c	12	64	3.4	49	8	AZ506149
c	13	64	3.4	49	8	AZ656875
c	14	64	3.4	49	8	AZ764533
c	15	64	3.4	49	8	AZ773388
c	16	64	3.4	49	8	AZ820100
c	17	64	3.4	49	9	TA168G09Q
c	18	64	3.4	50	4	BI491464
c	19	64	3.4	50	7	CV304274
c	20	64	3.4	50	8	AZ358097
c	21	64	3.4	50	8	AZ456166
c	22	64	3.4	50	8	AZ787456
c	23	64	3.4	50	8	AZ816605
c	24	64	3.4	50	8	AZ861629
c	25	64	3.4	50	8	AZ967786
c	26	64	3.4	50	9	BX987794
c	27	64	3.4	50	9	CR03825
c	28	64	3.4	50	9	CR025955
c	29	64	3.4	50	9	CR033162
c	30	64	3.4	50	9	CR048038
c	31	64	3.4	50	9	CR085382
c	32	64	3.4	50	9	CR122615
c	33	63	3.3	49	1	AI931428
c	34	63	3.3	49	8	AZ335579
c	35	63	3.3	49	8	AZ826077
c	36	62	3.2	39	8	AZ826077
c	37	62	3.2	42	9	TA63A10P
c	38	62	3.2	44	8	AZ342202
c	39	62	3.2	46	8	AZ981881
c	40	62	3.2	50	9	CR155014
c	41	61	3.2	48	8	AZ652813
c	42	60.5	3.2	50	9	CR117295
c	43	60	3.1	33	8	AZ627977
c	44	60	3.1	35	8	AZ317100
c	45	60	3.1	37	8	AZ369295

ALIGNMENTS

RESULT 1  
AA145482  
LOCUS  
DEFINITION  
AA145482 49 bp mRNA linear EST 11-FEB-1997  
mr62a06.r1 Stratagene mouse testis (#937308) Mus musculus CDNA  
clone IMAGE:602002 5', similar to TR:G307311 G307311 HISTONE H4. ;,  
mRNA sequence.

ACCESSION  
AA145482 GI:1714857

VERSION  
EST.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:367434  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev1 ET from Amersham



Db	47	GAAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAA	3
RESULT	5		
LOCUS	CR041958/c		
DEFINITION	Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP150e03, genomic survey sequence.		
ACCESSION	CR041958		
VERSION	CR041958.1		
KEYWORDS	GSS: Genomic survey sequence; MICER.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 50) Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <a href="http://www.sanger.ac.uk/MICER">http://www.sanger.ac.uk/MICER</a>		
FEATURES	Location/Qualifiers		
source	1..50 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /clone="MHPP150e03" /clone_lib="MHPP"		
ORIGIN			

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Alignment Scores:
Pred. No.:      3.92e+04      Length:      50
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Percent Similarity: 46.4%    Conservative: 1
Best Local Similarity: 42.8%  Mismatches:  3
Query Match:      3.46%     Indels:       12
DB:               9         Gaps:          1

US-09-544-776-2 (1-373) x CR041958 (1-50)
QY      143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       50 CCCCCCCCCCCCCCCCCCCCCC-----CCCCC 27

QY      163 AlaProAlaProAlaAlaProPro 170
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       26 CCCCCCCCCCCTCCCTCCCCCCCC 3

RESULT 6
AZ861612
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ861612
2M0168P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0168P16 F, genomic survey sequence.
AZ861612
AZ861612.1 GI:13058106
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

```

REFERENCE  
AUTHORS  
1. (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

UNIVERSITY OF UTAH  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT



JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE	22755829
PUBMED	12874060
REFERENCE	2
AUTHORS	Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE	23117147
PUBMED	14756321
REFERENCE	3
AUTHORS	Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL	Biotechniques 35 (6), 1164-1168 (2003)
PUBMED	14682050
REFERENCE	4 (bases 1 to 50)
AUTHORS	Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE	Direct Submission
JOURNAL	Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT	This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source form which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ Location/Qualifiers  source 1..50 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702" /clone="GK-366A11-017045" /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN	
Alignment Scores:	
Pred. No.:	4.55e+04 Length: 50
Score:	65.00 Matches: 12
Percent Similarity:	42.86% Conservatives: 0
Best Local Similarity:	42.86%
Query Match:	3.40% Indels: 12
DB:	Gaps: 1
US-09-544-776-2 (1-373) x BX002655 (1-50)	
Qy	. 143 ProProProProAlaSerValSerProGlInAGluProValTrpThrProPro 162       CCCCCCC
Dd	48 CCCCCCCCCCCCCCCCCCC-----CCCTTC 25
Qy	163 AlaProAlaProAlaProPro 170     
Dd	24 CCCCCCNCCNCCCCCCCCCCCC 1
RESULT 10	
CRI54670/c	
LOCUS	CRI54670 Reverse strand read from insert in 3'HPRT insertion targeting and DEFINITION CR154670 50 bp DNA linear GSS 06-JUL-2004





University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0347 row: J column: 05  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 49.

## FEATURES

1. 49  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0347005"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
Pred. No.: 5.16e+04 Length: 49  
Score: 64.00 Matches: 12  
Percent Similarity: 42.86% Conservative: 0  
Best Local Similarity: 42.86% Mismatches: 4  
Query Match: 3.35% Indels: 12  
DB: 8 Gaps: 1

US-09-544-776-2 (1-373) x AZ506149 (1-49)

QY 143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162  
Db 2 CCCCCCCCCCCCCCCCCC-----CCCCC 25  
QY 163 AlaProAlaProAlaAlaProPro 170  
Db 26 CCCCCCCCCCCCCCTCCCCCCCC 49

## RESULT 13

AZ656875  
LOCUS  
DEFINITION 49 bp DNA linear GSS 14-DEC-2000  
1M0532M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0532M11 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 49)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0532 row: M column: 11  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 49.

## FEATURES

## Source

## Location/Qualifiers

1. 49

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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
Pred. No.: 5.16e+04 Length: 49  
Score: 64.00 Matches: 12  
Percent Similarity: 42.86% Conservative: 0  
Best Local Similarity: 42.86% Mismatches: 4  
Query Match: 3.35% Indels: 12  
DB: 8 Gaps: 1

US-09-544-776-2 (1-373) x AZ656875 (1-49)

QY 143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162  
Db 1 CCCCCCCCCCCCCCCCCC-----CCCCC 24

QY 163 AlaProAlaProAlaAlaProPro 170  
Db 25 CCCCCCCCCCCCCCCCCCCCCC 48

## RESULT 14

AZ764533

LOCUS

DEFINITION 49 bp DNA linear GSS 16-FEB-2001  
1M0560017R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

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VERSION        AZ764533.1  GI:12879593
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 49)
               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0560 row: O column: 17
               Seq primer: CACACAGGAACAGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 49.
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               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
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               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.:      5.16e+04      Length:      49
Score:          64.00        Matches:    12
Percent Similarity: 42.86%    Conservative: 0
Best local Similarity: 42.86%
Query Match:    3.35%        Indels:     12
DB:             8            Gaps:       1

US-09-544-776-2 (1-373) x AZ764533 (1-49)

QY      143 ProProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
Db      1 CCCCCCCCCCCCCCCCCC-----CCCCC 24

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clone UUGC1M0560017 R, genomic survey sequence.
ACCESSION      AZ773388
VERSION        AZ773388
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 49)
               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0584 row: E column: 23
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               Class: plasmid ends
               High quality sequence stop: 49.
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               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.:      5.16e+04      Length:      49
Score:          64.00        Matches:    12
Percent Similarity: 42.86%    Conservative: 0
Best local Similarity: 42.86%
Query Match:    3.35%        Indels:     12
DB:             8            Gaps:       1

US-09-544-776-2 (1-373) x AZ773388 (1-49)

QY      163 AlaProAlaProAlaProPro 170
Db      25 CCCCCCCCCCCCCCCCCC-----CCCCC 48

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Best Local Similarity: 42.86% Mismatches: 4  
 Query Match: 3.35% Indels: 12  
 DB: 8 Gaps: 1

US-09-544-776-2 (1-373) x AZ773388 (1-49)

Qy	143	ProProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro	162
Db	1	CCCCCCCCCCCCCCCCCCCC-----CCCCC	24
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Search completed: August 4, 2005, 02:03:21  
 Job time : 3091 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:14:22 ; Search time 206 Seconds  
(without alignments)

2962.773 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLOSPLVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRAE 373

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	68	3.6	48	4	US-09-517-849-36
4	66	3.5	48	3	Sequence 36, Appl
5	66	3.5	48	3	US-09-580-923-34
6	66	3.5	50	3	Sequence 34, Appl
7	63	3.3	50	3	US-08-860-038-17
8	63	3.3	50	3	US-09-580-923-17
9	63	3.3	50	4	US-08-956-171E-2153
10	59	3.1	50	3	Sequence 17, Appl
11	59	3.1	45	3	US-08-781-986A-2153
12	59	3.1	45	4	Sequence 14, Appl
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13	58	3.0	38	1	US-08-563-864-1	Sequence 1, Appl
14	58	3.0	38	5	PCT-US95-06839-1	Sequence 1, Appl
15	57	3.0	39	1	US-08-068-747-9	Sequence 9, Appl
16	57	3.0	45	4	US-09-590-211A-9	Sequence 9, Appl
17	57	3.0	48	3	US-09-580-923-34	Sequence 34, Appl
18	57	3.0	48	4	US-09-119-507B-78	Sequence 78, Appl
19	57	3.0	48	4	US-08-897-556A-78	Sequence 78, Appl
20	57	3.0	48	4	US-09-547-693-78	Sequence 78, Appl
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22	57	3.0	50	3	US-09-580-923-17	Sequence 17, Appl
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36	53	2.8	33	4	US-09-590-211A-5	Sequence 5, Appl
37	53	2.8	35	4	US-09-196-270-10	Sequence 10, Appl
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39	53	2.8	36	4	US-09-590-211A-6	Sequence 6, Appl
40	53	2.8	39	1	US-08-068-747-9	Sequence 9, Appl
41	53	2.8	39	4	US-09-590-211A-7	Sequence 7, Appl
42	53	2.8	40	3	US-09-476-256-29	Sequence 29, Appl
43	53	2.8	42	4	US-09-590-211A-8	Sequence 8, Appl
44	53	2.8	43	3	US-09-411-722-4	Sequence 4, Appl
45	53	2.8	43	4	US-09-855-266A-4	Sequence 4, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-979-608A-36  
; Sequence 36, Application US/08979608A  
; Patent No. 6355451

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/979,608A

APPLICATION DATA:

FILING DATE: 26-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965



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; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
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; TOPOLOGY: linear
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; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-17

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Query Match: 3.46% Indels: 0
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US-09-544-776-2 (1-373) x US-08-860-038-17 (1-50)

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RESULT 6
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; Sequence 17, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wils, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-17

Alignment Scores:
Pred. No.: 1.29e+03 Length: 50
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Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 3.46% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-580-923-17 (1-50)

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DB 4 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 48
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RESULT 7

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HYPOTHETICAL: NO  
ANTI-SENSE: NO  
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RESULT 15  
US-08-068-747-9/c  
Sequence 9, Application US/08068747  
Patent No. 5695933  
GENERAL INFORMATION:  
APPLICANT: Schalling, Martin  
APPLICANT: Hudson, Thomas J.  
APPLICANT: Housman, David E.  
TITLE OF INVENTION: Direct Determination of Expanded  
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/068,747  
FILING DATE: 28-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-6141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Synthetic"

US-08-068-747-9  
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Db 37 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2

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Job time : 208 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 3, 2005, 17:14:22 ; Search time 686 Seconds  
(without alignments)  
3519.226 Million cell updates/sec

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Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 8279544

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	68	3.6	48	13	US-10-023-523-36	Sequence 36, Appl
5	68	3.6	48	17	US-10-616-187-36	Sequence 36, Appl
6	68	3.6	48	18	US-10-671-242-36	Sequence 36, Appl
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C 12	60	3.1	50	14	US-10-195-071-14	Sequence 14, Appl
C 13	60	3.1	50	19	US-10-627-253A-369	Sequence 369, App
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C 24	57	3.0	45	21	US-10-889-263-9	Sequence 9, Appl
C 25	57	3.0	45	21	US-10-831-819-14	Sequence 14, Appl
C 26	57	3.0	47	19	US-10-627-253A-373	Sequence 373, App
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C 29	57	3.0	48	17	US-10-437-708-78	Sequence 78, Appl
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C 42	54	2.8	36	19	US-10-296-085A-74	Sequence 74, Appl
C 43	54	2.8	42	10	US-09-833-203-8	Sequence 8, Appl
C 44	54	2.8	42	10	US-09-833-203-9	Sequence 9, Appl
C 45	54	2.8	42	15	US-10-211-296-11	Sequence 11, Appl

ALIGNMENTS

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; Sequence 36, Application US/09962055  
; Patent No. US20020052033A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; Lees, Robert S.  
; Law, Simon W.  
; Artjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.









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; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-195-072-14

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; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

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; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
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; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208

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; TYPE: DNA
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US-09-789-386-5

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QY 41 GluGluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGlu 60
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DB 901 AAGTTTGCAGTGTGTGATGGGTATTTACTATGTTGGTGGCTTGTATATGGTCTGACA 960
QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340
DB 961 CTACTGATTTTGGCTCTCACTTTCACTTTCACTTTCACTTTCTCTGTTTATTTATGAACG 1020
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
DB 1021 GCACAGATAGATCAATTATCTAGGACTTGCAAAATAGAATGTTAAAGATGCTATGGCTAA 1080
QY 361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
DB 1081 ATCCAAAGCAAAATCCCTGGATTGAAGCCAAAGCTGAA 1119

RESULT 2
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-09-765-205-5

Alignment Scores:
Pred. No.: 1,01e-158 Length: 1610
Score: 1879.00 Matches: 370
Percent Similarity: 99.20% Conservatives: 0
Best Local Similarity: 99.20% Mismatches: 3
Query Match: 98.38% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-09-765-205-5 (1-1610)
QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
DB 132 ATGGAAGACCTGGACAGCTCTCTCTGGTCTCGTCTCGGACAGCCACCCCGGCGCGAG 191
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
DB 192 CCGCGCTTCAAGTACCAGTTCTGTGGGAGCCCGAGGAGGAGGAGGAGGAG 251
QY 41 GluGluGluAspGluAspGluAspGluGluGluGluGluGluGluGluGluGlu 60
DB 252 GAAGAGGAGGACGAGGACGAGGACCTGGAGGAGCTGGAGGAGTGTCTGAGAGGAGCCGCG 311
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
DB 312 GCCGGGCTGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 371
QY 81 PheGlyAsnAspPheValProProAlaProAlaProArgGlyPheLeuProAlaAlaProVal 100
DB 372 TTCGGAATGACTTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 431
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
```

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Db 432 GCCCGGAGCGGAGCGCGTCTTGAGACCGGAGCGCGTCTGCTCGACCGTCCCGGCCA 491
QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
Db 492 TCCCGCGTGTCTGCTGCGCGAGTCTGCGCTCCAGCTCCAGAGCAGCAGCGCTCCG 551
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTTPThr 160
Db 552 GCCCGGCTCCCGCTCTCCCGCGCGCAGGTGAGCGCCCGCAGCAGCGCGTGTGACC 611
QY 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly 180
Db 612 CCGCCAGCGCGCGTCCCGCGCGCGCGCTCCACCGCGCGCGCGCCAGCGCAGCGGC 671
QY 181 SerSerGlySerValValValAspLeuLeuTyrTTPArgAspLysLysThrGlyVal 200
Db 672 TCTCGGCTCAGTGTGTGTGACCTCTCTGTACTGGAGACATTAAGAAGACTGGAGTG 731
QY 201 ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 220
Db 732 GTGTTGGTCCAGCTATTCTCTGCTGCTTTCATTGACAGTATTGAGCGTA 791
QY 221 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGly 240
Db 792 ACAGCTTACATTGCTTGGCGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGT 851
QY 241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260
Db 852 GTGATCAAGCTATCAAGAANTCAGATGAAGGCCACCCATTAGGGCATATCTGGAACT 911
QY 261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
Db 912 GAAGTTGCTATATCTGAGGAGTTGTTTCAAGGTACAGTAATCTCTGCTTGTGCTATGTC 971
QY 281 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeu 300
Db 972 AACTGCACGATAAAGGAACCTCAGCGCGCTCTCTTCTAGTGTATAGTTAGTTCTCTG 1031
QY 301 LysPheAlaValLeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
Db 1032 AAGTTGCGAGTGTGTGAGTGTATTTACTATGTTGGTCCCTGTTTAAATGCTTGACA 1091
QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340
Db 1092 CTACTGATTTTGGCTCTCACTTCTCAGTGTCTCTGTTTATGAACGCGATCAG 1151
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
Db 1152 GCACAGATAGATCATTTATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTAA 1211
QY 361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
Db 1212 ATCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 1250
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## RESULT 3

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US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication NO. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
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## US-10-347-669-5

## Alignment Scores:

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Pred. No.: 1,01e-158 Length: 1610
Score: 1879.00 Matches: 370
Percent Similarity: 99.20% Conservative: 0
Best Local Similarity: 99.20% Mismatches: 3
Query Match: 98.38% Indels: 0
DB: 21 Gaps: 0
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US-09-544-776-2 (1-373) x US-10-347-669-5 (1-1610)

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QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
Db 132 ATGGAAGACCTGGACCACTCTCTCTGCTCTCTCTCGACAGCCACCCGCGCGCAG 191
QY 21 ProAlaPheIstYrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
Db 192 CCGCGCTTCAAGTACCAGTTCTGTGAGGAGCCCGAGGAGGAGGAGGAGGAG 251
QY 41 GluGluGluAspGluAspGluAspLeuGluGluGluValLeuGluArgLysProAla 60
Db 252 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
Db 312 GCCGGCTGTCCGCGCGCCAGTGCACCGCGCTCTCGCGCGCGCGCGCTGATGGAC 371
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaProProVal 100
Db 372 TTCGAAATAGACTTCTGCGCGCGCGCGCGCGCGCGCGCGCTGCCCGCGCTCCCGCGTC 431
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
Db 432 GCCCGGAGCGGAGCGGCTCTTGGGACCGGCGCGCGCTGCTCGACGCGCGCGCGCA 491
QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
Db 492 TCCCGCTGTCTGCTCGCGCAGTCTCGCGCTCTCAAGCTCTCCAGGACGACGAGCGCTCCG 551
QY 141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTTPThr 160
Db 552 GCCCGGCTCTCCCGCTCTCCCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 611
QY 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly 180
Db 612 CCGCGAGCGCGCGCTCCCGCGCGCGCTCCACCGCGCGCGCGCGCGCGCGCGCG 671
QY 181 SerSerGlySerValValValAspLeuLeuTyrTTPArgAspLysLysThrGlyVal 200
Db 672 TCTCGGCTCAGTGTGTGTGACCTCTCTGCTCTCTGAGAGACATTAAGAAGACTGGAGTG 731
QY 201 ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 220
Db 732 GTGTTGGTGGCAGCGCTATTCTCTGCTGCTTTCATTGACAGTATTGAGCGTA 791
QY 221 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGly 240
Db 792 ACAGCTTACATTGCTTGGCGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGT 851
QY 241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260
Db 852 GTGATCAAGCTATCAAGAANTCAGATGAAGGCCACCCATTAGGGCATATCTGGAACT 911
QY 261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
Db 912 GAAGTTGCTATATCTGAGGAGTTGTTTCAAGGTACAGTAATCTCTGCTTGTGCTATGTC 971
QY 281 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeu 300
Db 972 AACTGCACGATAAAGGAACCTCAGCGCGCTCTCTTCTAGTGTATAGTTAGTTCTCTG 1031
QY 301 LysPheAlaValLeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
```

Db	1032	AGCTTTGCAGTGTGATGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCTGACA	1091	
Qy	321	LeuLeuIleLeuAlaIleSerLeuPheSerValProValIleTyrGluArgHisGln	340	
Db	1092	CTACTGATTTTGGCTCTCATTTTCACCTCTTCAGTGTTCCTGTTTATTAATGAACGGCATCAG	1151	
Qy	341	AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys	360	
Db	1152	GCACATAGATCATTTATCTAGGACTTGCAAAATPAGAAATGTTAAAGATGCTATGGCTAAA	1211	
Qy	361	IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu	373	
Db	1212	ATCCAGCAAAATCCCTGGATTGAAGCGCAAGACTGAA	1250	
RESULT 4				
US-10-956-157-4530				
; Sequence 4530, Application US/10956157				
; Publication No. US20050118625A1				
; GENERAL INFORMATION:				
; APPLICANT: Wyeth				
; APPLICANT: Mounts, William				
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH				
; FILE REFERENCE: 031896-043000 (AM 101081)				
; CURRENT APPLICATION NUMBER: US/10/956,157				
; CURRENT FILING DATE: 2004-10-04				
; NUMBER OF SEQ ID NOS: 319805				
; SOFTWARE: Patentin version 3.2				
; SEQ ID NO 4530				
; LENGTH: 2050				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-956-157-4530				
Alignment Scores:				
Pred. No.:	1.4e-158	Length:	2050	
Score:	1879.00	Matches:	370	
Percent Similarity:	99.20%	Conservative:	0	
Best Local Similarity:	99.20%	Mismatches:	3	
Query Match:	98.38%	Indels:	0	
DB:	21	Gaps:	0	
US-09-544-776-2 (1-373) x US-10-956-157-4530 (1-2050)				
Qy	1	MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln	20	
Db	67	ATGGAAGACCTGACACAGTCTCCTCTGGTCTCGTCTCGACAGCCACCCCGCGCGAG	126	
Qy	21	ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu	40	
Db	127	CCGCGTTTCAGTACCATGTTCTGTAGGGAGCCGACGAGACGAGGAGAGAGAGAG	186	
Qy	41	GluGluGluAspGluAspGluLeuGluGluLeuGluValLeuGluArgLysProAla	60	
Db	187	GAAGAGGAGGACGAGCAGCAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAGCCCGCC	246	
Qy	61	AlaGlyLeuSerAlaIleProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80	
Db	247	GCGGGCTGTGCGCGCCCGCAGTGCCACCGCCCTGCGCGCGCGCGCCCTGATGGAC	306	
Qy	81	PheGlyAsnAspPheValProProAlaProAlaProAlaGlyPheLeuProAlaProVal	100	
Db	307	TTCGGAAATGACTTCGTGTCGCGCGCGCGCGCGCGCGCGCGCGCTGCCCGCCGCT	366	
Qy	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120	
Db	367	GCCCCGAGCGGACGCGCTTTGGGACCGAGGCGCGGTGCTGCGACCGTGCCTCCCGGCCA	426	
Qy	121	SerPheLeuSerAlaAlaIleValSerProSerLysLeuProGluAspAspGluProPro	140	
Db	427	TCCCGCTGTGCTGCCCGAGTCTCGCCCTCCAGCTCCCTGAGGACGACGAGCCTCG	486	

Qy	141	AlaAtgProProProProProAlaSerValSerProGlnAlaGluProValTTPThr	160	
Db	487	GCCGGCCTCCCCCTCCTCCCGCGCAGGTGAGCCCGCCAGCAGAGCCCGTGTGACC	546	
Qy	161	ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly	180	
Db	547	CCGCCAGCCCGGCTCCCGCGCGCCCTCCACCCCGCGCGCCCAAGCGCAGGGGC	606	
Qy	181	SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	200	
Db	607	TCCTCGGGCTCAGTGGTGTTCACCTCTCTGTACTTGGAGAGACATTAAAGAACTGAGTG	666	
Qy	201	ValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal	220	
Db	667	GTGTTGGTGGCCAGCTATTCCTGCTCTTCATTGACAGATTCAGCAATTTGACCGTA	726	
Qy	221	ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly	240	
Db	727	ACAGCCTACATTTGCCCTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCT	786	
Qy	241	ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer	260	
Db	787	GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT	846	
Qy	261	GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal	280	
Db	847	GAAGTTGCTATATCTGAGGAGTTGGTTCAGAGTAGTACAGTAATCTGCTCTTGGTCATGTG	906	
Qy	281	AsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu	300	
Db	907	AACTGCACGATAAAGAACTCAGGGCCCTCTCTTAGTTGATGATTTAGTTCTCTCTG	966	
Qy	301	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	320	
Db	967	AAGTTTGCAGTGTGATGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACA	1026	
Qy	321	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln	340	
Db	1027	CTACTGATTTTGGCTCTCATTTTCATCTTCAGTGTTCCTGTTTATTAAGACGGCATCAG	1086	
Qy	341	AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys	360	
Db	1087	GCACAGATAGATCATTTCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAA	1146	
Qy	361	IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu	373	
Db	1147	ATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA	1185	
RESULT 5				
US-10-956-157-4531				
; Sequence 4531, Application US/10956157				
; Publication No. US20050118625A1				
; GENERAL INFORMATION:				
; APPLICANT: Wyeth				
; APPLICANT: Mounts, William				
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH				
; FILE REFERENCE: 031896-043000 (AM 101081)				
; CURRENT APPLICATION NUMBER: US/10/956,157				
; CURRENT FILING DATE: 2004-10-04				
; NUMBER OF SEQ ID NOS: 319805				
; SOFTWARE: Patentin version 3.2				
; SEQ ID NO 4531				
; LENGTH: 2226				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-956-157-4531				
Alignment Scores:				
Pred. No.:	1.56e-158	Length:	2226	
Score:	1879.00	Matches:	370	
Percent Similarity:	99.20%	Conservative:	0	
Best Local Similarity:	99.20%	Mismatches:	3	





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QY 161 ProProAlaProAlaProAlaProSerThrProAlaAProLysArgArgGly 180
|||
Db 622 CCGCCAGCCCGGCTCCCGCGGCCCTCCACCCCGCGCGCCCAAGCGCAGGGC 681
|||
QY 181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200
|||
Db 682 TCTCGGGCTCAGTGGTGTGTGACCTCCTGTACTGGAGAGACATTAAAGAACTGGAGTG 741
|||
QY 201 ValPheGlyValAspSerLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220
|||
Db 742 GTGTTTGGTGCAGGCTATTCTCTGCTGCTTTCATTGACAGTATTCAGCAATTGTGAGCGTA 801
|||
QY 221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly 240
|||
Db 802 ACAGCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGT 861
|||
QY 241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260
|||
Db 862 GTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCT 921
|||
QY 261 GluValAlaIleSerGluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
|||
Db 922 GAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTCTTGGTCAATGTG 981
|||
QY 281 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
|||
Db 982 AACTGCAGATTAAGGAATCAGGCGCCTCTCTTCTAGTTGATGATTTAGTTGATCTCTCG 1041
|||
QY 301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
|||
Db 1042 AAGTTTGCAAGTGTGATGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACA 1101
|||
QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340
|||
Db 1102 CTACTGATTTTGGCTCTCATTTCACTCTTCACTGTTTCTCTGTTATTATTAAGCGCATCAG 1161
|||
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
|||
Db 1162 GCACGATAGATCATTAATCTAGACTTGCATTAATAGAAATGTAAGATGCTATGGCTAAT 1221
|||
QY 361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
|||
Db 1222 ATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 1260
|||
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## RESULT 7

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US-10-466-258-3
; Sequence 3, Application US/10466258
; Publication NO. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1188)
US-10-466-258-3
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## Alignment Scores:

Pred. No.:	7,31e-158	Length:	2052
Score:	1871.00	Matches:	368
Percent Similarity:	98.93%	Conservatives:	1
Best Local Similarity:	98.66%	Mismatches:	4
Query Match:	97.96%	Indels:	0
DB:	19	Gaps:	0

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US-09-544-776-2 (1-373) x US-10-466-258-3 (1-2052)
QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20
|||
Db 67 ATGGAAGACCTCGACAGTCTCTCTGGTCTCTCGACAGCCACCCCGCGCGCAG 126
|||
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
|||
Db 127 CCCGGTTCAGTACAGTTCTGTGAGGAGCCCGAGGACGAGGAGGAGGAGGAG 186
|||
QY 41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
|||
Db 187 GAAGAGGAGGACGAGGACGAGACCTCGAGGAGCTGGAGTCTCTGAGAGGAAGCCCGCC 246
|||
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
|||
Db 247 GCCGGGCTGTCCGCGGCCCAAGTGCACCGCCCTGCGCGCGCGCGCCCTGATGGAC 306
|||
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
|||
Db 307 TTCGGAATGACTTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCCCGGTC 366
|||
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
|||
Db 367 GCCCGGAGCGGCACGCGGTGTGGGACCCGAGCCCGGTGTCTGACCGTGCCTCGGCCA 426
|||
QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140
|||
Db 427 TCCCCGCTGTCTGTGCGCGCAGTCTCGCCCTCCAAGCTCCCTCAGGACGACGAGCTCCG 486
|||
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
|||
Db 487 GCCCGGCTTCCCCCTCTCTCCCGCGCAGCGTGAGCCCCCAGGACGAGCCCTGTGGACC 546
|||
QY 161 ProProAlaProAlaProProSerThrProAlaAProLysArgArgGly 180
|||
Db 547 CCGCCAGCCCGGCTCCCGCGCGCCCTCCACCCCGCGCGCCCAAGCGCAGGGGC 606
|||
QY 181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200
|||
Db 607 TCTCGGGCTCAGTGGTGTGTGACCTCTCTGTACTGAGAGACATTAAGAAGACTCGAGTG 666
|||
QY 201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220
|||
Db 667 GTGTTTGGTGCAGGCTATTCTCTGTCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTA 726
|||
QY 221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly 240
|||
Db 727 ACAGCCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGT 786
|||
QY 241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260
|||
Db 787 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCT 846
|||
QY 261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
|||
Db 847 GAAGTTGCTATATCTGAGGAGTTGGTTTCAAGAGTACAGTAATTCCTCTTGGTCAATGTG 906
|||
QY 281 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
|||
Db 907 AACTGCAGCAATAAGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATCTCTG 966
|||
QY 301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
|||
Db 967 AAGTTTGCAGTGTTCATGGGTATTTACCTATGTTGGTGCCTTGTAAAGGCTGACA 1026
|||
QY 321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340
|||
Db 1027 CTACTGATTTTGGCTCTCATTTCACTCTCTGAGTGTCTCTGTTATTATTAAGCGCATCAG 1086
|||
QY 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
|||
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US-09-544-776-2 (1-373) x US-10-205-194-165 (1-2782)	
QY	1 MetGluAspLeuAspGlnSerProLeuValSerSerSer---AspSerProProArgPro 19
Db	701 ATGGAAGACATAGACACAGTCGTGGTCTCTCTGCTCCACGACAGCCGCCCGCGCT 760
QY	20 GlnProAlaPheIysTyrGlnPheValArgGluProGluAspGlucluu---GluGluGlu 38
Db	761 CCGCCCGCTTCAAGTACCAGTTCGTGACGGAGCCGAGGACGAGGAGGAGGAG 820
QY	39 GluGluGluGluAspGluAspGluAspLeuGluGluGluValLeuGluArgLys 58
Db	821 GAGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 880
QY	59 ProAlaAlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeu 78
Db	881 CCGCAGCCGGGTGTCCGAGCTGGGTGGCG-----CCGCGCCGCCCGCGCGCTG 934
QY	79 MetAspPheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaPro 98
Db	935 CTGGACTTCAGCAGGACACTCGGTGCCCCCGCGCCCGCGCGCGCGCGCGCGCC 994
QY	99 ProValAlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValPro 118
Db	995 CCGCGCGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1045
QY	119 AlaProSerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGlu 138
Db	1046 GCGCCATCGCTGCGCGCGCTGCGCGAGTCTGCGCTCCAGCTCCAGGAGGAGGAG 1105
QY	139 ProProAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
Db	1106 CTCCCGCGAGGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1159
QY	159 TrpThrProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArg 178
Db	1160 -----CCG 1198
QY	179 ArgGlySerSer----- 182
Db	1199 AGGGGCTCCGGCTCAGTGGATGAGACCCCTTTTGGCTCTCTGCTGATCTGAAACCTGTG 1258
QY	183 -----GlySerValValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyVal 200
Db	1259 ATACCTCTCTGACGTTGTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTG 1318
QY	201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220
Db	1319 GTGTTGGTGCACGCTATTCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGA 1378
QY	221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly 240
Db	1379 ACGGCTACATTGCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGCG 1438
QY	241 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260
Db	1439 GTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCAATTAGAAATCT 1498
QY	261 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
Db	1499 GAAGTTGCTATATCAGAGGAATGGTTTCAGAAATACAGTAATTTCTGCTCTTGGTCATGTG 1558
QY	281 AsnCysThrIleLysGlnLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
Db	1559 AACACACAAATAAAGAACTGAGCGCGCTTTTCTTAGTTGATGATTTAGTTATTCCTCTG 1618
QY	301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
Db	1619 AAGTTTGCAGTGTGTGATGGGTGTTACTATGTGGTGCCTTGTTCATGGTCTGACA 1678
QY	321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 340
Db	1679 CTACTGATTTTGTAGCTCTGATCTCACTCTTCACTATTCTTGTTATTATTGAACGGCATCAG 1738
QY	341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
Db	1739 GTGCAGATAGATCATTTATCTAGACTTGCAACAACAAGAGTGTTAAGGATGCCCAAA 1798
QY	361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
Db	1799 ATCCAAGCAAAANTCCCTGGATTGAAGCGCAAGCAGAT 1837
RESULT 10	
US-09-789-386-1	
; Sequence 1, Application US/09789386	
; Patent No. US20020010324A1	
; GENERAL INFORMATION:	
; APPLICANT: MICHALOVICH, DAVID	
; APPLICANT: PRINJHA, RABINDER KUMAR	
; TITLE OF INVENTION: NOVEL COMPOUNDS	
; FILE REFERENCE: GP-30165-C1	
; CURRENT APPLICATION NUMBER: US/09/789,386	
; CURRENT FILING DATE: 2001-02-21	
; PRIOR APPLICATION NUMBER: U.K. 9916898.1	
; PRIOR FILING DATE: 1999-07-19	
; PRIOR APPLICATION NUMBER: U.K. 9816024.5	
; PRIOR FILING DATE: 1998-07-22	
; PRIOR APPLICATION NUMBER: US 09/359,208	
; PRIOR FILING DATE: 1999-07-22	
; NUMBER OF SEQ ID NOS: 6	
; SOFTWARE: FastSeq for Windows Version 3.0	
; SEQ ID NO 1	
; LENGTH: 3579	
; TYPE: DNA	
; ORGANISM: HOMO SAPIENS	
US-09-789-386-1	
Alignment Scores:	
Pred. No.:	1,38e-120 Length: 3579
Score:	1459.50 Matches: 370
Percent Similarity:	31.04% Conservative: 0
Best Local Similarity:	31.04% Mismatches: 3
Query Match:	76.41% Indels: 819
DB:	9 Gaps: 1
US-09-544-776-2 (1-373) x US-09-789-386-1 (1-3579)	
QY	1 MetGluAspLeuAspGlnSerProLeuValSerSerSerSerSerSerProProArgProGln 20
Db	1 ATGGAAGACCTGGACAGTCTCTCTGCTCTCTCGACAGCCACCCCGCGCGCAG 60
QY	21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
Db	61 CCGCGTTCAGATCACAGTTCTGAGGAGGCCCGGAGGAGGAGGAGGAGGAGGAG 120
QY	41 GluGluGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
Db	121 GAAGAGGAGGACGAGGACGAGACCTGGAGGAGCTGGAGGTCTGAGAGGAAGCCCGCC 180
QY	61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
Db	181 GCCCGGCTGTCCGCGCGCCCAAGTGCACCCCTCGCGCGCGCGCGCGCTGATGGAC 240
QY	81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
Db	241 TTCGGAATGATCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCCCGCTC 300
QY	101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
Db	301 GCCCGGAGGCGCAGCCGTCTGGGACCGAGCCCGGTGTCTGACCGGTGCGCGCGCCA 360
QY	121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
Db	361 TCCCGCTGTCTGCTGCGCGCGCTCTCGCCCTCCAAAGTCCCTTGAGGAGCAGCGCTCCG 420



Db 2581 GATTCACTCCAATTGAATTATAGATGAGTTCCTTACATTGATCAGTTCTTAAACTGAT 2640  
QY 185 ----- 185  
Db 2641 TCATTTTCTAAATTAGCCAGGAATATACTGACCTAGATATCCCAAAAGTGAAAT 2700  
QY 185 ----- 185  
Db 2701 GCTAATGCCCGGATGGAGCTGGTCAATTCGCTTGACAGAAATGGCCCATGACCTTTCT 2760  
QY 185 ----- 185  
Db 2761 TTGAAGAACATACAACCCAAAGTTGAAGAGAAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820  
QY 185 ----- 185  
Db 2821 AATGGGTCTGCTACATCAAAAGTGCTCTTATTGCTCCAGATGTTTCTGCTTTGGCCACT 2880  
QY 185 ----- 185  
Db 2881 CAAGCAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAGAACTGAGAAAAA 2940  
QY 185 ----- 185  
Db 2941 CTTCTCTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTG 3000  
QY 186 -----ValValAspLeuLeuTyrTrpArgAspIleIysIysThrGlyValVal 201  
Db 3001 AGTAAACTTCAGTTGTTGACCTCTGTAAGAGACATTAAGAAGACTGGAGTGGTG 3060  
QY 202 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221  
Db 3061 TTTGGTGCAGCCTATTCTCTGCTTTTCATTGACAGTATTGACGATTTGTGAGCGTAACA 3120  
QY 222 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrIysGlyVal 241  
Db 3121 GCCTACATTTGCCCTTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTG 3180  
QY 242 IleGlnAlaIleGlnIysSerAspGlyGlyHisProPheArgAlaTyrIleuGluSerGlu 261  
Db 3181 ATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGAA 3240  
QY 262 ValAlaIleSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsn 281  
Db 3241 GTTGCTATATCTGAGAGTGTGGTTGAGAAGTACAGTAATCTGCTTGGTCATGTGAAC 3300  
QY 282 CysThrIleGlyGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIys 301  
Db 3301 TGCACGATAAAGAACTCAGGGCGCTCTTCTTAGTTGATGATTTAGTTCTCTGAAG 3360  
QY 302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleu 321  
Db 3361 TTTGCAGTGTGATGGGTATTTACCTATGTTGGTGCTTGTTAATGGTCTGACACTA 3420  
QY 322 LeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 341  
Db 3421 CTGATTTTGGCTCTCATTTTCATCTTCAGTGTCTGTTATTATGAAGGATCAGGGC 3480  
QY 342 GlnIleAspHisTyrLeuGlyLeuAlaAsnIysAsnValIysAspAlaMetAlaIysIle 361  
Db 3481 CAGATAGATCATTATCTAGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAAAATC 3540  
QY 362 GlnAlaIleProGlyLeuIysArgIysAlaGlu 373  
Db 3541 CAAGCAAAAAATCCCTGGATTGAAGCGCAAAAGCTGAA 3576

RESULT 11

US-09-893-348-22

; Sequence 22, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
; OTHER INFORMATION:  
US-09-893-348-22

Alignment Scores:

Pred. No.: 1.38e-120 Length: 3579  
Score: 1459.50 Matches: 370  
Percent Similarity: 31.04% Conservative: 0  
Best Local Similarity: 31.04% Mismatches: 3  
Query Match: 76.41% Indels: 819  
DB: 9 Gaps: 1

US-09-544-776-2 (1-373) x US-09-893-348-22 (1-3579)

QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20  
Db 1 ATGGAAGACCTGGACAGTCTCTCTGGTCTCGTCTCGGACAGCCACCCCGGCGCAG 60  
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40  
Db 61 CCCGGTTCAGTACCACTTCGTGAGGAGGCCCGGAGGACGAGGAGGAAGAGAGGAG 120  
QY 41 GluGluGluAspGluAspGluLeuGluLeuGluValLeuGluArgGlyProAla 60  
Db 121 GAAGAGGAGGACGAGGACGAGACCTGGAGGAGCTGGAGGTCTGGAGAGGAGCCGCC 180  
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
Db 181 GCCGGGTGTGCGCGGCCCGCAGTGCACCGCCCTGCGCGCGCGCGCCCTGATGAC 240  
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProVal 100  
Db 241 TTCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCGCGTC 300  
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120  
Db 301 GCCCGGAGCGGACACCGCTCTTGGGACCGGACCGCGGTGTCGTGACCGTGTCCCGCCA 360  
QY 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140  
Db 361 TCCCGCTGTCTGCTGCGCGCAGTCTCGCCCTCCAGCTCCCTGAGGACGACGAGCTCG 420  
QY 141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160  
Db 421 GCCCGCTCTCCCTCTCTCCCGCGCCAGCGGTGAGCGGACCGCCAGGACGAGCCGTGTGAC 480  
QY 161 ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProIysArgGly 180  
Db 481 CGCCAGCCCGCGGTCTCCCGCGCGCCCTCTCCACCCCGCGCGCGCCCAAGCGAGGGGC 540

[illegible]

Db	1621	GAAGTCGTGGCAAAACATGTCCTGAAGCCTGACTCCAGATTTAGTACAGGAAGCANTGTGAA	1680
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Db	1681	AGTGAAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAACACAAAAATGAGCTTGGTT	1740
Qy	185	-----	185
Db	1741	CAAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCAGCAGCTTTGCCCATCATTT	1800
Qy	185	-----	185
Db	1801	GAAGAGTCAGAAGCTACTCTCTTACCAGTTTTGCTTGACATTGTTATGTAAGACCACTTG	1860
Qy	185	-----	185
Db	1861	AAATTCTGCAGTTCTAGTGTGCTGGTTCCTGATACAGCCAGCTCATCACCATTAGAA	1920
Qy	185	-----	185
Db	1921	GCTTCTTCAGTTAATTATGAAGCATAAAACATGAGCCTGAAAACCCCCCACCATATGAA	1980
Qy	185	-----	185
Db	1981	GAGGCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCT	2040
Qy	185	-----	185
Db	2041	GAATAATTAATGCAGCTCTTCAAGAAACAGAGCTCCTTATATATCTATTGTCATGTGAT	2100
Qy	185	-----	185
Db	2101	TTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTCCTGTATTATTCAGAA	2160
Qy	185	-----	185
Db	2161	ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTTGAAGATTCTCACCCT	2220
Qy	185	-----	185
Db	2221	GATTCGNAACCAAGTTGACTTATTTAGTGTGATTCATATCACTGACGTTCCCAAAAACAA	2280
Qy	185	-----	185
Db	2281	GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGATGTCATGATA	2340
Qy	185	-----	185
Db	2341	GAATATGMAAATAAGGAAAAAAGTCTGCTTTGCCACTGAGGAGGAAAGCCATATTG	2400
Qy	185	-----	185
Db	2401	GAATCTTTTAAGCTCAGTTTAGATAACACAAAGATACCCTGTTACCTGTATGAAGTTCA	2460
Qy	185	-----	185
Db	2461	ACATTGACAAAAAGGAGAAAAATTCCTTTGCAGATGGAGAGCTAGTACTGCAGTTTAT	2520
Qy	185	-----	185
Db	2521	TCAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAACTGAAACGTTTTCA	2580
Qy	185	-----	185
Db	2581	GATTCATCTCCAATTGAAATTAAGATGAGTTCCCTCATTTGATCAGTTCTTAAAACTGAT	2640
Qy	185	-----	185
Db	2641	TCATTTTCTAAATTAGCCAGGGAATATATGACCTTAGAGTATCCCAAAAAGTGAATTT	2700
Qy	185	-----	185

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Db 2701 GCTAATGCCCGGATGGAGCTGGGTCAATTGCCCTTGACAGAAATTGCCCATGACCTTTCT 2760
QY 185 ----- 185
Db 2761 TTGAAGAACATACAAACCAAGTTGAAGAGAAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820
QY 185 ----- 185
Db 2821 AATGGGTCTGCTACATCAAAAGGTGCTCTATTGCGCTCCAGATGTTTCTGCTTGGCCACT 2880
QY 185 ----- 185
Db 2881 CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTAAGAAAGCTGAGAAAAA 2940
QY 185 ----- 185
Db 2941 CTTCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTTCAGCAGAGCTG 3000
QY 186 -----ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal 201
Db 3001 AGTAACAACCTTCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGT 3060
QY 202 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221
Db 3061 TTTGGTGCAGCCTATTCTCTGCTGCTTTCAATTGACAGTATTGAGCATTTGTGAGCGTAACA 3120
QY 222 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGlyVal 241
Db 3121 GCCTACATTGGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATATACAAGGGTGT 3180
QY 242 IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 261
Db 3181 ATCCAGACTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAATCTGAA 3240
QY 262 ValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 281
Db 3241 GTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCGTCTTGCTCATGTGAAC 3300
QY 282 CysThrIleLysGluLeuArgGluPheLeuValAspIleValAspSerLeuLys 301
Db 3301 TGACACATAAAGAACTCAGAGCGCCTCTCTTAGTTGATGATTAGTTGATTTCTTGAAG 3360
QY 302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321
Db 3361 TTTGCAGTGTGATGTGGGTATTACTATGTGGTGCCTTGTTTAATGCTGACACTA 3420
QY 322 LeuIleAlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAla 341
Db 3421 CTGATTTTGGCTCTCATTTTCACCTCTTCAGTGTTCCTGTTATTATTATGAACGGCATCAGGCG 3480
QY 342 GlnIleAspHisTyrIleuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 361
Db 3481 CAGATAGATCATTTATCTAGACTTGCATAATAAGAATGTTAAAGATGCTATGCTAAATC 3540
QY 362 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
Db 3541 CAAGCAAAAATCCCTGGATTGAAGCCAAAGCTGAA 3576
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## RESULT 12

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US-10-267-502-212
; Sequence 212, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-212
Alignment Scores:
Pred. No.: 1,38e-120 Length: 3579
Score: 1459.50 Matches: 370
Percent Similarity: 31.04% Conservative: 0
Best Local Similarity: 31.04% Mismatches: 3
Query Match: 76.41% Indels: 819
DB: 18 Gaps: 1
US-09-544-776-2 (1-373) x US-10-267-502-212 (1-3579)
QY 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerSerProProArgProGln 20
Db 1 ATGGAAGACCTGGACAGCTCTCTGTGCTCTGTCCTCGACAGCCACCCCGGCGCAG 60
QY 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGlu 40
Db 61 CCGCGGTTCAGTACAGTTCGTGAGGAGGCCCGGAGGACGAGGAGGAGAGAGAG 120
QY 41 GluGluGluAspGluAspIleAspLeuGluLeuGluValLeuGluArgLysProAla 60
Db 121 GAAGAGGAGGACGAGGACGAAAGACCTGGAGGAGCTGGAGGTCTGGAGAGGAA 180
QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
Db 181 GCCCGGCTGTCCGCGGCCCCAGTGTGCCACCGCCCTGCGCGCGCGCGCTGTATG 240
QY 81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProVal 100
Db 241 TTCGGAATATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCTCCCGCGTC 300
QY 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
Db 301 GCCCGGAGCGGACGCGCTCTTGGGACCGGACCGAGCCCGGTGTGTGTGACCG 360
QY 121 SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspGluProPro 140
Db 361 TCCCGCGCTGTGTGCGCGAGTCTGCGCCTTCAAGCTCCCTGAGGACGACGAGCT 420
QY 141 AlaArgProProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
Db 421 GCCCGGCTCCCGCTCTCCCGCGGACGAGTGTGAGCCCGCGGACGAGCCCGT 480
QY 161 ProProAlaProAlaProProProProProProAlaProProSerThrProAlaAlaProLysArgGly 180
Db 481 CCGCCAGCCCGGCTCCCGCGCGCGCGCGCTCCACCCCGCGCGCGCGCGCGAGG 540
QY 181 SerSerGlySerVal----- 185
Db 541 TCCTCGGCTCAGTGGATGAGAGACCTTTTGTCTTCTGTCGATCTGTAGCCTGTG 600
QY 185 ----- 185
Db 601 CGCTCCTCTGCAGAAAAATATGGACTTGAAGGAGCAGCCAGGTAAACACTATTTCGGTGT 660
QY 185 ----- 185
Db 661 CAAGAGGATTTCCCATCTGCTGTTGAAACTGCTGCTTCTTCTTCTTCTCTGTC 720
QY 185 ----- 185
Db 721 CTCTCAGCGCTTCTTTCAAAGAACATGAATACCTTGGTGAATTTGTCAACAGTATTAC 780
QY 185 ----- 185
Db 781 ACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTTAAAGAGGTCTCAGAGAGGCA 840
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Db 961 GAAGAAATAATCGTGAATAATAAAGATGAAGAAGAGAAAGTTAGTTAGTAATAACATCCTT 1020  
QY 185 ----- 185  
Db 1021 CATAATCAACAGAGTTACCTACAGCTCTTACTAAATTTGGTTAAAGAGATGAAGTTGTG 1080  
QY 185 ----- 185  
Db 1081 TCCTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAAAGCTCCTATG 1140  
QY 185 ----- 185  
Db 1141 AGGAGGAATATGCAGACTTCAAAACCAATTTGAGCGAGTATGGGAAGTGAAGATAGTAAG 1200  
QY 185 ----- 185  
Db 1201 GAAGATAGTATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTGGAAAGTAAAGTG 1260  
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Db 1261 GATAAAAAATGTTTTCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTAGAGT 1320  
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Db 1321 AGTAATGATGATACTTCTTTCCCAAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380  
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Db 1441 CCTTTGTAGGAGATCCTACTTCAGAAAAATAAGACCGTGAAAAAATAAGAAAG 1500  
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QY 185 ----- 185  
Db 1561 GCAGCACAGGATTCAGACAGATTTATGTCAACACAGATTAATTAACAAGGTGACTGAG 1620  
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Db 1621 GAAAGTCGTGCAAAACATGCTGAAGGCTGACTCCAGATTTAGTACAGGAAGCATGTGA 1680  
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Db 1681 AGTGAATTCGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTT 1740  
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Db 1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCTCGCAGCAGAGCTTTGGCCCATCATTT 1800  
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Db 1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTCCTGACATTTGTTATGGAAGCACCATTG 1860  
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QY 185 ----- 185  
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QY 185 ----- 185  
Db 2161 ATGGCAAAAGTTGAACAGCCAGTGCCTGATCACTCTGAGCTAGTTGAAGATTCTCACCT 2220  
QY 185 ----- 185  
Db 2221 GATTTCTGAACCAAGTTGACTTATTTTAGTGATGATTTCAATACCTGACGTTCCACAAAACAA 2280  
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Db 2281 GATGAACCTGTGATGCTTGTGAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA 2340  
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Db 2581 GATTCATCTCCAATTGAAATTTAGATGAGTTCCCTACATTTGATGATGATCTTCAAACTGAT 2640  
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QY 185 ----- 185  
Db 2761 TTGAAGAACATACAAACCCAAAGTTGAAGAGAAAAATCAGTTTCTCAGATGACTTTCTAAA 2820  
QY 185 ----- 185  
Db 2821 AATGGGTCTGTACATCAAAAGGTGCTCTTATTGCTCTCAGATGTTTCTGCTTTGGCCACT 2880  
QY 185 ----- 185  
Db 2881 CAAGCAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAGAAGCTGAGAAAAAA 2940  
QY 185 ----- 185  
Db 2941 CTTCTCTCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTTCAGCAGAGCTG 3000  
QY 186 ----- 186  
Db 3001 AGTAAACCTTCAGTTGTTGACCTCTCTGTAAGAGACATTAAGAAAGCTGGAGTGGTG 3060  
QY 202 PheGlyAlaSerIleuPheLeuSerLeuThrValPheSerIleValSerValThr 221

3061	Db		TTTTGGTCCAGCCATTTCCTGCTGCTTTCAATGTGACAGTATTCAGCATTTGTGAGCGTAACA	3120
222	Qy		AlaTyrlleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrlsGlyVal	241
3121	Db		GCCTACATTCGCTTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAGGGHGTG	3180
242	Qy		IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlsGluSerGlu	261
3181	Db		ATCCAAGCTATTCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAA	3240
262	Qy		ValAlaIleSerGluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsn	281
3241	Db		GTTTGCTATATCTGAGGAGTTGGTTTCAAGAAGTACAGTAATTTCTGCTCTTGGCTATGTGAAC	3300
282	Qy		CysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys	301
3301	Db		TGCACGATAAAGNACTCAGCGGCTCTTCTTAGTTGATGATTAGTGTGATTTCTCTGAG	3360
302	Qy		PheAlaValLeuMetTrpValPheThrTyrlsValGlyAlaLeuPheAsnGlyLeuThrLeu	321
3361	Db		TTTTCAGTGTGATGTGGTATTTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACTA	3420
322	Qy		IleIleLeuAlaIleLleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAla	341
3421	Db		CTGATTTTGGCTCTCATTTTCACTCTTCAGTGTGCTCTGTTATTTATGAACGGCATCAGCG	3480
342	Qy		GlnIleAspHisTyrlsLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle	361
3481	Db		CAGNATAGTCATTTATCTAGGACTTGCAATAAGNATGTTTAAGNATGCTATGGCTAAATC	3540
362	Qy		GlnAlaLysIleProGlyLeuLysArgLysAlaGlu	373
3541	Db		CAAGCAAAATTCCTCGATTGAACGCGAAAGCTGAA	3576

RESULT 13  
US-10-327-213--8  
; Sequence 8, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

FILE REFERENCE: CONY/003  
CURRENT APPLICATION NUMBER: IIS/10/327 213

; CURRENT APPLICATION NUMBER: US/I  
 : CURRENT FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 43

; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.1

; SOFTWARE: FACEHUNT VER. 2.1  
; SEQ ID NO 8

LENGTH: 3579

TYPE: DNA

**ORGANISM: Homo sapiens**

US-10-327-213-8

**Alignment Scores:**

Pred. No.: 1.38e-

Score: 1459.5

Percent Similarity: 31.04%

Best Local Similarity: 31.04%

Query Match: 76.41%

DB: 19

115-08-544-776-2 (1-373) ~ 115-1

US-09-544-116-2 (1-3/3) X US-1

Qy 1 MetG]11AspI.e111AyrG

QY I M E T G I W A S P L E N A S P O

Db  
1 ATGGAAGACCTGGACC

[illegible]

Qy 21 ProAlaPheLysTyrG

\_\_\_\_\_

Db 61 CCCGCGTTCAAGTACC

Qy	41	GluGluGluAspGluAspGluAspLeuGluGluLeuValLeuGluArgLysProAla	60
Db	121	GAAGAGGAGGACGAGGACGAAGACCTGGAGAGCTGGAGGTGCTGGAGAGGAAGCCGCC	180
Qy	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
Db	181	GCCGGGCTGTCCGGCGCCGAGTGCCACCGCCCCCTGCCCGCGCGCCCCCTGATGGAC	240
Qy	81	PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal	100
Db	241	TTCCGAATGACTTCGTGCGCGCGCGCCCGGGACCCCTGCCGGCGGCTCCCCCGTC	300
Qy	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
Db	301	GCCCGGAGGGCAGCGCTCTTGGGACCCGAGCCCGGTGCTGCGACCGTGCCCGCGCCA	360
Qy	121	SerPheLeuSerAlaAlaValSerProSerLysLeuProGluAspAspGluProPro	140
Db	361	TCCCGCTGTCTGTCGGCAGTCTCGCCCTCAAGCTCCCTGAGGACGAGAGCTTCG	420
Qy	141	AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
Db	421	GCCCGGCTCCCGCTCTCCCGCGGCAGCGTGAGCCCCCAGGACGCGGTGTGGACC	480
Qy	161	ProProAlaProAlaProAlaProProSerThrProAlaProLysArgArgGly	180
Db	481	CCGCCAGCCCGGCTCCCGCGCGCCCTCCACCCCGCGCGCCCAAGCGAGGCGGC	540
Qy	181	SerSerGlySerVal	185
Db	541	TCCTCGGCTCAGTGGATGAGACCTTTTGTCTTCTCTGTCATCTGAGCCTGTGATA	600
Qy	185		185
Db	601	CGTCTCTGCAGAAAAATATGGACTTGAAGGAGCAGCAGTAACATAATTCGGTGGT	660
Qy	185		185
Db	661	CAAGAGATTTCCATCTGTCTGCTTGAAACTGCTCTTCTCTCTCTCTCTCTCTCT	720
Qy	185		185
Db	721	CTCTCAGCGCTTCTTTCAAAGAACATGAATACTTGGTAAATTTGTCAACAGTATTACCC	780
Qy	185		185
Db	781	ACTGAAGGAACACTTCAAGAAAATGTCACTGAAGCTTCTAAAGAGGTCTCAGAGAAGCA	840
Qy	185		185
Db	841	AAAACCTCTACTCATAGATAGAGATTTAAACAGAGTTTTTCAGAAATTAGAATACTCAGAAATG	900
Qy	185		185
Db	901	GGATCATCGTTACGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCAAAATCTTAGG	960
Qy	185		185
Db	961	GAGGAATAATCGTGAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAATAACATCCTT	1020
Qy	185		185
Db	1021	CATAATCAACAAGATTACCTACAGCTCTTACTAAATTTGGTTAAAGAGGATGAAGTTGTG	1080
Qy	185		185
Db	1081	TCCTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAGCTCCTATG	1140
Qy	185		185
Db	1141	AGGAGGAATATGCAGACTTCAAACCACTTTGAGCGAGTATGGGAAGTGAAGAAGATAGTAAG	1200

QY 185 ----- 185  
Db 1201 GAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTGGAAAGTAAAGTG 1260  
QY 185 ----- 185  
Db 1261 GATAAAATGTTTTCAGATAGCTTGGAGCAAACTAATCAGAAAGATAGTGAGAT 1320  
QY 185 ----- 185  
Db 1321 AGTAATGATGATACTTCTTTCCCGTAGTACCCAGAGGTATAAGGATCGTCCAGGACA 1380  
QY 185 ----- 185  
Db 1381 TATATCACATGTGCTCCCTTTAAACCCAGCAGCAACTGAGAGCATTTGCAACAAACATTTT 1440  
QY 185 ----- 185  
Db 1441 CCTTTGTTAGGAGATCTTCTCAGAAAATAAGACCGATGAAAAAATAAGAGAAAG 1500  
QY 185 ----- 185  
Db 1501 AAGGCCAATAGTAACAGAGAGAGATACTAGCACCAACATCAAAACCTTTTCTTGTA 1560  
QY 185 ----- 185  
Db 1561 GCAGCACAGGATTTCTGAGACAGATTATGTCAACACAGATAATTTAAACAAAGGTGACTGAG 1620  
QY 185 ----- 185  
Db 1621 GAAGTCGTGCAAAACATGCTGAGAGCTGCTGAGGCTGCTCCAGATTTAGTACAGGAAGCATGAA 1680  
QY 185 ----- 185  
Db 1681 AGTGAATTGAATGAACTTACTGTGTAACAAGATTGCTTATGAACAAAATGGACTTGGTT 1740  
QY 185 ----- 185  
Db 1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCTGTCAGCACAGCTTTGCCCCATCATTT 1800  
QY 185 ----- 185  
Db 1801 GAAGAGTCAGAAGTACTCCTTACCAGTTTTCGCTGACATTTGTTATGGAAGCACCATTG 1860  
QY 185 ----- 185  
Db 1861 AATTCTGCAGTTCTCTAGTGTGGTGCTTCCGTGATACAGCCAGCTCATCACCATTAGAA 1920  
QY 185 ----- 185  
Db 1921 GCTTCTTCAGTTAATTATGAAGCATAAACATGAGCCTGAAAAACCCCCACCATATGAA 1980  
QY 185 ----- 185  
Db 1981 GAGGCCATGAGTGATACACTAAAAAAGTATCAGGAATAAGAGAAATTAAGAGCCT 2040  
QY 185 ----- 185  
Db 2041 GAAATATTAATGCAGCTCTTCAAGAAACAGAGCTCCTTATATATCTATTGTCATGTAT 2100  
QY 185 ----- 185  
Db 2101 TTAATTAAGAAAAAAGCTTTTCTGCTGAAACAGCTCCGGATTCTCTGTATTATTCAGAA 2160  
QY 185 ----- 185  
Db 2161 ATGGCAAAAGTTGAACAGCAGTGCCTGATCATTTCTGAGCTAGTTGAAGATTCCTCACCT 2220  
QY 185 ----- 185  
Db 2221 GATTCGAAACAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAAACAA 2280  
QY 185 ----- 185

Db 2281 GATGAACACTGTGATGCTTGTGAAGAAAGTCTCACTGAGACTTCAATTGAGTCAATGATA 2340  
QY 185 ----- 185  
Db 2341 GAATATGAANAATAAGAAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAGCCATATTTC 2400  
QY 185 ----- 185  
Db 2401 GAATCTTTTAAGCTCAGTTTAGATACACAAAAAGATACCCTGTTACCTGATGAAGTTTCA 2460  
QY 185 ----- 185  
Db 2461 ACATTGAGCAAAAAGGAGAAAAATTCCTTTGAGATGAGGAGCTCAGTACTGCAGTTTAT 2520  
QY 185 ----- 185  
Db 2521 TCAATGATGACTTATTATTATTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA 2580  
QY 185 ----- 185  
Db 2581 GATTCACTCCAAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTTAAACCTGAT 2640  
QY 185 ----- 185  
Db 2641 TCATTTTCTAAATTAGCCAGGGAATATCTGACCTAGAAAGTATCCACAAAAGTGAAAT 2700  
QY 185 ----- 185  
Db 2701 GCTAATGCCCGATGGAGCTGGTCAATTGCTTGCAAGAAATGGCCCATGACCTTTCT 2760  
QY 185 ----- 185  
Db 2761 TTGAAGAACATACAAACCCAAAGTTGAAGAGAAAAATCAGTTTCTCAGATGACTTTCTTAA 2820  
QY 185 ----- 185  
Db 2821 AATGGGTCTGTACATCAAAAGGTGCTTATTGCTCCAGATGTTTCTGCTTTGGCCACT 2880  
QY 185 ----- 185  
Db 2881 CAAGCAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAGCTGAGAAAAA 2940  
QY 185 ----- 185  
Db 2941 CTTCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTTCAGCAGAGCTG 3000  
QY 186 ----- 186  
Db 3001 AGTAAAACTTCAGTTTGTTCACCTCCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTG 3060  
QY 186 ----- 186  
Db 3061 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221  
QY 186 ----- 186  
Db 3061 TTTGGTCAGGCTATTCTCTGCTTTCATTCAGCAGTATTCAGCATTTGTGAGCGTAACA 3120  
QY 186 ----- 186  
Db 3121 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProargIleTyrIleVal 241  
QY 186 ----- 186  
Db 3121 GCCTACATTGGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTG 3180  
QY 186 ----- 186  
Db 3181 IleGlnAlaIleGlnIleSerSerAspGluGlyHisProPheArgAlaTyrIleGluSerGlu 261  
QY 186 ----- 186  
Db 3181 ATCCAGCTATCCAGAAATCAGATGAAGGCCACCCCATCAGGGCATATCTGGAATCTGAA 3240  
QY 186 ----- 186  
Db 3241 ValAlaIleSerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsn 281  
QY 186 ----- 186  
Db 3241 GTTGTATATCTGAGAGGTGGTTTCAAGAGTACAGTAATCTGCTCTTGGTCATGTGAAC 3300  
QY 186 ----- 186  
Db 3301 CysThrIleIleGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIle 301  
QY 186 ----- 186  
Db 3301 TGCACGATAAAGAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTGATTTCTCTGAAG 3360  
QY 186 ----- 186  
Db 3302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321

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Db      3361  TTTCAGTGTGATGTGGGTATTACCTATGTTGGTGCCCTGTTAAATGGTCTGACACTA 3420
Qy      322  LeuileLeuAlaLeuileSerLeuPheSerValProValiletYrGluArqHisGlnAla 341
Db      3421  CTGATTTTGGCTCTCATTTCACTTCTTCAGTGTTCCTGTTATTTATGACCGCATCAGCG 3480
Qy      342  GlnleAspHisTyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysile 361
Db      3481  CAGATAGATCATTTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATC 3540
Qy      362  GlnAlaLysileProGlyLeuLysArgLysAlaGlu 373
Db      3541  CAAGCAAAAATCCCTGGATTGAAGCGCAAAAGCTGAA 3576

RESULT 14
US-10-466-258-8
; Sequence 8, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
US-10-466-258-8

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Qy	161	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys	Arg	Gly	180	
Db	481	CCG	CC	AC	CGG	CGT	CC	CG	CG	CG	CC	CC	CC	CC	CC	CC	CG	CG	CG	540	
Qy	181	Ser	Ser	Gly	Ser	Val	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	541	TC	CT	CGG	CT	CAG	TGG	ATG	AG	AC	CC	TTT	TG	CT	CT	CT	CT	GC	AT	600	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
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Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
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Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	721	CT	CT	C	G	CG	G	T	T	CT	CA	A	A	A	C	A	T	G	A	780	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	781	ACT	G	A	G	G	A	A	C	ACT	T	C	A	G	T	G	A	G	G	840	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	841	A	A	A	A	C	T	A	C	T	A	T	A	A	C	A	G	A	G	900	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	901	G	G	A	T	C	A	T	C	A	T	G	T	CT	CT	C	A	A	A	960	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	961	G	A	G	A	A	A	A	T	A	A	G	A	T	A	A	G	A	G	1020	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1021	C	A	T	A	T	C	A	A	C	A	G	T	T	A	C	T	T	A	1080	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1081	T	C	T	T	C	A	A	A	A	A	G	A	C	A	G	T	T	A	1140	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1141	A	G	G	A	G	A	T	A	T	G	C	A	G	A	T	T	G	G	1200	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1201	G	A	G	A	T	A	T	G	T	T	G	G	T	C	T	T	A	A	1260	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1261	G	A	T	A	A	A	A	A	T	G	T	T	G	C	A	T	A	A	1320	
Qy	185	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	185	
Db	1321	A	G	T	A	T	G	A	T	A											

Db 1501 AAGGCCCAATAGTAACAGAGAGAATACTAGCACCAAAACATCAAAACCCCTTTTCTTGTA 1560  
QY 185 ----- 185  
Db 1561 GCAGCAGAGATTCTGAGACAGATTATGTCAACAAGATTAATTAACAAGAGTGACTGAG 1620  
QY 185 ----- 185  
Db 1621 GAAGTCGTGCAACATGCCTGAAGGCCTGACTCCAGATTAGTACAGGAAGCATGTGAA 1680  
QY 185 ----- 185  
Db 1681 AGTGAATTGAATGAATTACTGTGTACAAAGATTGCTTATGAACAATAATGGACTTGGTT 1740  
QY 185 ----- 185  
Db 1741 CAACATCAGAAGTTATGCAAGAGTCACTATCTCTGCAGCAGACTTTGGCCCATCATTT 1800  
QY 185 ----- 185  
Db 1801 GAAGAGTCAGAAGCTACTCTTACCAGTTTTCCTGCTGACATTGTTATGGAGCACCATTG 1860  
QY 185 ----- 185  
Db 1861 AATTCTGCAGTTCTTAGTGTGCTTCCGTGATACAGCCCACTCATCACCATTAGAA 1920  
QY 185 ----- 185  
Db 1921 GCTTCTTCAGTTAATTATGAAGCATAAACATGAGCCTGAAACCCCCACCATATGAA 1980  
QY 185 ----- 185  
Db 1981 GAGGCCATGAGTATCACTAAATAAAGTATCAGGAATAAGGAATAAAGAGCCT 2040  
QY 185 ----- 185  
Db 2041 GAAATATATTAAATGAGCTCTTCAAGAAACAGAGCTCTTATATATCTATTGTCATGTAT 2100  
QY 185 ----- 185  
Db 2101 TTAATTAAGAAACAAAGCTTCTGTGAACAGCTCCGGATTCTCTGATTAATTCAGAA 2160  
QY 185 ----- 185  
Db 2161 ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTTGAAGATTCTCACCT 2220  
QY 185 ----- 185  
Db 2221 GATTCTGAACCACTGACTTATTTAGTGATGATTAATCAATACCTGACGTTCCACAAAAACAA 2280  
QY 185 ----- 185  
Db 2281 GATGAACCTGTGATGCTTGTGAAGAAAGTCTCACTGAGACTTCAATTTGAGTCAATGATA 2340  
QY 185 ----- 185  
Db 2341 GAATATGAAAATAAGGAAAACCTCAGTGTCTTCCACCTGAGGGAGGAAGCCATATTG 2400  
QY 185 ----- 185  
Db 2401 GAATCTTTAAGCTCAGTTAGATTAACAAAAAGATACCTGTTACCTGTATGAAGTTTCA 2460  
QY 185 ----- 185  
Db 2461 ACATTGAGCAAAAGGAGAAAATTCCTTTGAGATGGAGAGCTCAGTACTGACGTTTAT 2520  
QY 185 ----- 185  
Db 2521 TCAAATGATGACTTATTTATTTCTAAGGAAGCAGACATAAGAGAACTGAAAGCTTTTCA 2580  
QY 185 ----- 185

Db 2581 GATTCATCTCCAATTGAAATTTATAGATGAGTTCCCTACATTTGATCAGTTCTTAAACATGAT 2640  
QY 185 ----- 185  
Db 2641 TCATTTTCTAAATTAGCCAGGGAAATATCTGACCTAGAAGTATCCCAAAAAGTGAAAT 2700  
QY 185 ----- 185  
Db 2701 GCTAATGCCCCGATGGAGTGGTTCATTGGCTTTGCACAGAAATGGCCCATGACCTTTCT 2760  
QY 185 ----- 185  
Db 2761 TTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820  
QY 185 ----- 185  
Db 2821 AATGGGTCTGTACATCAAAAGGTGCTTATTTGCCCTCCAGATGTTTCTGCTTTGGCCACT 2880  
QY 185 ----- 185  
Db 2881 CAAGCAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAGAAGCTGAGAAAAA 2940  
QY 185 ----- 185  
Db 2941 CTTCTTCCGATACAGAAAAAGAGGACAGATCACCATCTCTATATTTTTCAGCAGAGCTG 3000  
QY 186 -----ValValAspLeuLeuTyrTpaGAspIleLysThrGlyValVal 201  
Db 3001 AGTAAACTTCAGTTGTTGACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTG 3060  
QY 202 PheGlyValSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221  
Db 3061 TTTGGTGCAGCCTATTCTCTGCTGCTTTCATTGACAGATTTACAGATTGTGAGCGTAACA 3120  
QY 222 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerProArgIleTyrLysGlyVal 241  
Db 3121 GCCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATATACAAGGGTGTG 3180  
QY 242 IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 261  
Db 3181 ATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAACTCTGAA 3240  
QY 262 ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 281  
Db 3241 GTTGCTATATCTGAGAGTTGGTTCAAGAAGTACAGTAATTCGTCTCTGCTCATGTGAAC 3300  
QY 282 CysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLys 301  
Db 3301 TGCACGATAAAGGAACCTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTCTCTGAAG 3360  
QY 302 PheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321  
Db 3361 TTTGCAAGTTGATGTGGGTATTTACCTATGTTGGTCTTGTATTTATGCTGACACTA 3420  
QY 322 LeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 341  
Db 3421 CTGATTTTGCCTCTCATTTCTCTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGCG 3480  
QY 342 GlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 361  
Db 3481 CAGATAGATCATTTATCTAGGACTTGCAAATAGAATGTTAAAGATGCTATGGCTAAATTC 3540  
QY 362 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373  
Db 3541 CAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 15

US-10-810-653-22  
; Sequence 22, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
; OTHER INFORMATION:  
US-10-810-653-22

## Alignment Scores:

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Percent Similarity: 31.04% Conservative: 0  
Best Local Similarity: 31.04% Mismatches: 3  
Query Match: 76.41% Indels: 819  
DB: 20 Gaps: 1

US-09-544-776-2 (1-373) x US-10-810-653-22 (1-3579)

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QY 21 ProAlaPheIysTyrGlnPheValArgGluProGluAspGluGluGluGlu 40  
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QY 41 GluGluAspGluAspGluAspLeuGluGluValLeuGluArgLysProAla 60  
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QY 61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80  
DB 181 GCGCGGCTGTGCGGCGCCAGTGTGCGCCACCGCCCTGCGCGCGCGCGCGCGCG 240  
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DB 241 TTCGGAATGACTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
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 Job time : 743 secs

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Total number of hits satisfying chosen parameters: 8279544

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	37.4	1.7	48	16	US-10-275-071-34
3	37.4	1.7	50	16	US-10-275-071-17
4	35.2	1.6	48	9	US-09-962-055-36
5	35.2	1.6	48	9	US-09-976-740-36
6	35.2	1.6	48	13	US-10-023-529-36
7	35.2	1.6	48	13	US-10-023-523-36

8	35.2	1.6	48	17	US-10-616-187-36	Sequence 36, Appl
9	35.2	1.6	48	18	US-10-671-242-36	Sequence 36, Appl
10	29.6	1.3	46	21	US-10-820-487-9	Sequence 9, Appl
11	29.6	1.3	46	21	US-10-903-975-9	Sequence 9, Appl
12	28.6	1.3	36	17	US-10-418-182-86	Sequence 86, Appl
13	28.6	1.3	36	21	US-10-479-472A-12	Sequence 12, Appl
14	28	1.2	45	9	US-09-962-055-30	Sequence 30, Appl
15	28	1.2	45	9	US-09-976-740-30	Sequence 30, Appl
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17	28	1.2	45	13	US-10-023-523-30	Sequence 30, Appl
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C 21	26.4	1.2	36	17	US-10-418-182-84	Sequence 84, Appl
C 22	26.4	1.2	36	19	US-10-296-085A-74	Sequence 74, Appl
C 23	25.8	1.2	30	13	US-10-101-487-2	Sequence 2, Appl
C 24	25.8	1.2	30	13	US-10-101-487-65	Sequence 65, Appl
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C 26	25.8	1.2	30	21	US-10-939-988-65	Sequence 65, Appl
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29	25.6	1.1	50	18	US-10-329-624-2153	Sequence 2153, Ap
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35	25.2	1.1	30	21	US-10-939-988-63	Sequence 27, Appl
36	25.2	1.1	50	10	US-09-306-333A-27	Sequence 4349, Ap
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38	25	1.1	25	19	US-10-717-597-4350	Sequence 4351, Ap
39	25	1.1	25	19	US-10-717-597-4351	Sequence 4352, Ap
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41	25	1.1	25	19	US-10-717-597-4353	Sequence 4354, Ap
42	25	1.1	25	19	US-10-717-597-4354	Sequence 4355, Ap
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45	25	1.1	25	19	US-10-717-597-4357	Sequence 4357, Ap

ALIGNMENTS

RESULT 1

US-10-131-827-743

; Sequence 743, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 743

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-743

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Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;











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4	37.4	1.7	50	6	AR167590	Sequence
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C 13	31	1.4	39	6	IB4408	Sequence 9
C 14	28.2	1.3	49	6	CQ002787	Sequence
15	28	1.2	36	6	A91851	Sequence 10
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**SOURCE**  
**ORGANISM**

**YOU  
FEATURE**

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Job time : 9532 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2005, 17:10:58 ; Search time 1182 Seconds  
(without alignments)  
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Title: US-09-544-776-1

Perfect score: 2240

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	34	1.5	42	4	AAF31000 Human NOG
8	34	1.5	43	4	AAF30999 Human NOG
9	32.4	1.4	42	10	ABZ22128 Polyanion
10	32.4	1.4	42	10	ABZ22092 Polyanion
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c	43	25	1.1	25	12	ADP17628	Adp17628 Renal cel
c	44	25	1.1	25	12	ADP17820	Adp17820 Renal cel
c	45	25	1.1	25	12	ADP17624	Adp17624 Renal cel

#### ALIGNMENTS

#### RESULT 1

ABZ00752

ID ABZ00752 standard; DNA; 50 BP.

AC ABZ00752;

XX

DT 09-JAN-2003 (first entry)

DE Human leukocyte gene expression profiling probe SEQ ID NO 743.

XX

XX

KW T7: leukocyte; gene expression profiling; allograft rejection;

KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;

KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

XX SS.

OS Homo sapiens.

XX

XX

PN WO200257414-A2.

XX

PD 25-JUL-2002.

XX

PF 22-OCT-2001; 2001WO-US047856.

XX

PR 20-OCT-2000; 2000US-0241994P.

XX

PA 08-JUN-2001; 2001US-0296764P.

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XX

CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcomes, determining prognosis for a patient,  
 CC predicting disease complications in an individual or monitoring response  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX  
 SQ Sequence 50 BP; 13 A; 6 C; 13 G; 18 T; 0 U; 0 Other;  
 Query Match 2.2%; Score 50; DB 6; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 2140 TGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTGTGAACCTGT 2189  
 DB 1 TGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTGTGAACCTGT 50  
 XX  
 RESULT 2  
 ADG33274  
 ID ADG33274 standard; DNA; 50 BP.  
 XX  
 AC ADG33274;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human DNA probe used to monitor expression of diagnostic genes SeqID598.  
 XX  
 KW human; ss; autoimmune; chronic inflammatory disease; SLE;  
 KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;  
 KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;  
 KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;  
 KW diverticulitis; primary biliary sclerosis; probe.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003090694-A2.  
 XX  
 PD 06-NOV-2003.  
 XX  
 PF 24-APR-2003; 2003WO-US013015.  
 XX  
 PR 24-APR-2002; 2002US-00131827.  
 XX  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 XX  
 PI Wohlgemuth J, Fry K, Woodward R, Ly N;  
 XX  
 DR WPI; 2003-877243/81.  
 XX  
 PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
 PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
 PT colitis, psoriasis and asthma by detecting the expression level of one or  
 PT more genes.  
 XX  
 PS Claim 1; SEQ ID NO 598; 877pp; English.  
 XX  
 CC This invention relates to novel methods for diagnosing and monitoring  
 CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
 CC the identification of genes that have a clinical utility as diagnostic  
 CC tools for the management of, in particular, patients with systemic lupus  
 CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
 CC present invention describes a method for determining the levels of  
 CC multiple differentially expressed genes of a patient, in a concerted  
 CC manner, in order to achieve an improved diagnostic assay with sensitivity  
 CC and specificity for the disease in question. As such, these genes are  
 CC useful for the diagnosis of various other inflammatory disorders  
 CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
 CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
 CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
 CC This oligonucleotide is a human DNA probe used to monitor the expression

CC level of the differentially expressed diagnostic genes of the invention.  
 XX  
 SQ Sequence 50 BP; 13 A; 6 C; 13 G; 18 T; 0 U; 0 Other;  
 Query Match 2.2%; Score 50; DB 10; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 2140 TGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTGTGAACCTGT 2189  
 DB 1 TGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTGTGAACCTGT 50  
 XX  
 RESULT 3  
 AAS21106  
 ID AAS21106 standard; DNA; 48 BP.  
 XX  
 AC AAS21106;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE (GGA)16 DNA purification oligonucleotide.  
 XX  
 KW ss; DNA purification; triple helix; plasmid purification.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT repeat\_region 1..48  
 FT /\*tag= a  
 FT /rpt\_type= TANDEM  
 FT repeat\_unit 1..3  
 FT /\*tag= b  
 FT /note= "GAA repeat type"  
 XX  
 PN WO200192511-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US017122.  
 XX  
 PR 26-MAY-2000; 2000US-00580923.  
 XX  
 PA (AVET ) AVENTIS PHARMA SA.  
 XX  
 PI Crouzet J, Scherman D, Wills P, Blanche F, Cameron B;  
 XX  
 DR WPI; 2002-097772/13.  
 XX  
 PT Purifying double-stranded (ds) DNA from a solution containing dsDNA and  
 PT other components, comprises passing the solution through a support  
 PT comprising a covalently coupled oligonucleotide able to form a triple  
 PT helix with the dsDNA.  
 XX  
 PS Example 7; Page 20; 40pp; English.  
 XX  
 CC This invention comprises a method of purifying double-stranded DNA from a  
 CC solution containing the double-stranded DNA mixed with other components,  
 CC comprising passing the solution through a support comprising a covalently  
 CC coupled oligonucleotide capable of forming a triple helix with the double  
 CC -stranded DNA by hybridisation with a specific sequence present in the  
 CC double-stranded DNA. The method is useful for purifying double-stranded  
 CC DNA contained in a solution and mixed with other components. The new  
 CC method is a simple, rapid and effective method for DNA purification, and  
 CC makes it possible to obtain especially high purities with high yields.  
 CC The method enables DNA to be purified from complex mixtures comprising  
 CC other nucleic acids, proteins, endotoxins, nucleases and the like. The  
 CC supports may be readily recycled, and the DNAs obtained display improved  
 CC properties to pharmaceutical safety. Further, the method entails only one  
 CC step contrary to prior art. The present sequence represents a DNA  
 CC sequence contained within the plasmid pXL2725. This sequence is used for  
 CC purification of this plasmid using the method of the invention  
 XX

[illegible][illegible]









RESULT 15  
AAS13776

